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(54) Title: COMPUTER-ASSISTED MEANS FOR ASSESSING LIFESTYLE RISK FACTORS

(57) Abstract: The present invention relates to a computer assisted method of providing a personalized lifestyle advice plan for a human subject in which an individual's genotype is analysed for the presence of alleles at one or more genetic loci which may be associated with lifestyle risk factors, and the alleles present compared to a first dataset comprising information correlating the presence of individual alleles at genetic loci with a lifestyle risk factor to provide a risk factor associated with the presence of particular alleles in order to generate a personalized lifestyle advice plan. This may include for example recommended minimum and/or maximum amounts of food subtypes.

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Computer-Assisted Means For Assessing Lifestyle Risk Factors

Field of the Invention

The present invention relates to methods of assessing disease susceptibility. In particular, it relates to methods of assessing disease susceptibility associated with dietary and lifestyle risk factors.

Background to the Invention

Cancer is a disease influenced primarily by external factors. Up to 80% of human cancers arise from exposure to environmental agents. The majority of cancer is believed to be preventable because exposure to these external factors should be manageable (Giovannucci, 1999; Perera, 2000).

Human tumours result from a series of mutational events, leading to the loss of the regulatory mechanisms that govern normal cell behaviour and ultimately resulting in the formation of a tumour with full metastatic (or invasive) potential (Smith, 1995). All higher organisms have developed a complex variety of mechanisms to protect themselves from environmental insult, for example from ingested plant toxins. One of the most important protection measures involves the metabolism of toxins (or xenobiotics) leading to detoxification and ultimately excretion of the toxin (Smith, 1995). Unfortunately, the metabolic pathways do not always lead to detoxification of the toxin. Indeed many chemical carcinogens are activated by these same metabolic pathways to react with cellular macromolecules.

Improvements in genetic analysis and the availability of human

genetic sequence information arising from the Human Genome Project has added another facet to the analysis of cancer susceptibility, that of inter-individual variation at the genome level. Molecular epidemiology has already begun to clarify some of the gene-environment interactions that may lead to disease. The ultimate goal of molecular epidemiology is to develop risk assessment models for individuals, and already the field has provided insight into inter-individual variation in human cancer risk (Shields, 2000). Molecular epidemiology focuses on three major determinants of human cancer risk: inherited host susceptibility factors, molecular dosimetry of carcinogen exposure, and biomarkers of early effects of carcinogenic exposure. The variability in metabolic activity, detoxification and DNA repair of the US population could be as high as 85-500-fold with correspondingly high variability in cancer risk (Hattis, 1986). Considering the latency of cancer, the importance of correlating individual risk with biomarkers at an early stage becomes apparent. These biomarkers can help to identify populations or individuals at risk of cancer resulting from specific environment-gene interactions.

Defining the factors that contribute to inter-individual variations in cancer susceptibility has been a major focus of research for many years. Given the suggested role of environmental factors in carcinogenesis, some of the candidate genes are those that encode the xenobiotic-metabolising enzymes that activate or inactivate carcinogens. Variable levels of expression of these enzymes could result in increased or decreased carcinogen activation. Other genetic factors that could contribute to cancer susceptibility include genes involved in DNA repair, proto-oncogenes, tumour suppressor genes, cell-cycle genes, as well as genes involved

in aspects of nutrition, hormonal status, and immunological responses. Emerging data from the Human Genome Project has led to studies that show combinations of metabolic polymorphisms are increasingly being linked to a greater risk of cancer (Perera, 1997). Studies which have measured the formation of DNA adducts as a marker of enzyme activity have found that the levels of DNA damage or protein adducts vary considerably between persons with apparently similar exposure (Bryant, 1987; Perera, 1992; Mooney, 1995). The observed variability reflects a combination of true biologic factors, unaccounted for by differences in exposure or laboratory variation (Dickey, 1997). In fact, lower exposures to carcinogens can result in proportionately higher adduct levels because of a person's genetic predisposition for increased carcinogen metabolic activation (Kato, 1995; Vineis, 1997)

The existence of multiple alleles at loci that encode xenobiotic-metabolising enzymes can result in differential susceptibilities of individuals to the carcinogenic effects of various chemicals. Metabolism in humans occurs in two distinct phases: Phase I Metabolism involves the addition of an oxygen atom or a nitrogen atom to lipophilic (fat soluble) compounds such as steroids, fatty acids, xenobiotics (from external sources like diet, smoke, etc.) so that they can be conjugated to glutathione or N-acetylated by the Phase II enzymes (thus made water-soluble) and excreted from the body. There are superfamilies of xenobiotic-metabolising enzymes: cytochrome P450's (Phase I), GSTs (Phase II) and NATs (Phase I and II) which are thought to have evolved as an adaptive response to environmental insult. Alterations in the activity of these enzymes are predicted to result in an altered susceptibility to cancer (Hirvonen, 1999).

Enzymatic activation of xenobiotics is not, however, the only route to cancer development. Epidemiological studies suggest that nutritional factors may also play a causative role in more than 30% of human cancers. However, defining the precise roles of specific dietary factors in the development of cancer is difficult due to the multitude of variables involved (Perera, 2000). Specific dietary factors are not easily measured as a single quantifiable variable, such as number of cigarettes smoked per day. Further complications arise due to differences in methodology, control populations, types of carcinogens, and amounts of exposure to carcinogens.

Priorities for studies relating to the interrelationship of dietary factors and cancer susceptibility include identification of genetic factors that contribute to individual cancer risk, identification of cancer-preventative chemicals in fruits and vegetables, better understanding of carcinogenic role of polycyclic aromatic hydrocarbons and heterocyclic amines generated by cooking meats at high temperature, and better understanding of the role of increased caloric intake with increased cancer risk (Perera, 2000).

Increased consumption of vegetables and fruits is correlated with a decreased risk of cancer, and studies of this aspect of nutritional effects on cancer has led to the identification of other enzymes and micronutrients involved in the maintenance of a normal cellular phenotype (Giovannuci, 1999).

One quarter of the US population with low intake of fruits and vegetables has roughly twice the cancer rate for most types of cancer (lung, larynx, oral cavity, oesophagus, stomach, colon and rectum, bladder, pancreas, cervix, and ovary) when compared with the quarter with the highest intake (Ames,

1999). Fruit and vegetables are high in folate and antioxidants. Low intake can lead to micronutrient deficiency, which has been shown to cause DNA damage in a way that mimics radiation damage by causing single and double-stranded breaks, oxidative lesions or both. The micronutrients correlated with DNA-damaging activity include folate (or folic acid), iron, zinc, and vitamins B12, B6, C and E (Ames, 1999).

Of the cancers that are correlated with nutritional effects, colon cancer (colorectal neoplasia) has among the strongest links to diet. In the US, colon cancer is the fourth most common incident cancer and second most common cause of cancer death in the US, with 130,000 new cases and 55,000 deaths per year (Potter, 1999). According to the WHO, colorectal cancers are the second most common cause of cancer death in Britain (WHO, 1997). Worldwide colon cancer represents 8.5% of new cancer cases reported, with the highest rates seen in the developed world and the lowest rates in India. Colon cancer occurs with approximately equal frequency in men and women, and the occurrence appears to be highly sensitive to changes in the environment. Immigrant populations assume the incidence rates of the host country very rapidly, often within the generation of the initial immigrant (Potter, 1999).

Risk factors for colon cancer include a positive family history, meat consumption, smoking and alcohol consumption (Giovannuci, 1999). There is an inverse relationship, i.e. lower risk, associated with consumption of vegetables, high folate intakes, use of non-steroidal anti-inflammatory drugs, hormone replacement therapy and physical activity. Meat and tobacco smoke are sources of carcinogens, while vegetables are a source of folate, antioxidants, and have Phase II

(detoxifying) enzyme-inducing ability (Taningher, 1999).

Diets rich in raw vegetables, green vegetables, and cruciferous vegetables have a decreased risk of colon cancer. Diets high in fibre, from vegetables and cereals, have been associated with a greater than two-fold decrease in risk of colorectal adenomas in men. The data on fruit in the diet is not as consistent to date (WCRF, 1997), but a recent report (Eberhart, 2000) measured potent anti-oxidant activity of phytochemicals in apple skins with the ability to inhibit growth of tumour cell lines in vitro, so it is possible that more clearly defined links will emerge in the future. Lower risk of colon cancer is associated with high folate intakes, but actual consumption of vegetables, rather than specific micronutrient preparations or vitamin supplements, has the most consistent low risk (Potter, 1999).

Other cancers that have been correlated with nutrition include prostate and breast. These malignancies are largely influenced by a combination of factors related to diet and nutrition. Prostate cancer is associated with high consumption of milk, dairy products and meats. These products decrease levels of 1,25(OH)2 vitamin D, which is a cell differentiator. Low levels of 1,25(OH)2 vitamin D may enhance prostate carcinogenesis by preventing cells from undergoing terminal differentiation and continuing to proliferate (Giovannucci, 1999). Breast, colon, and prostate cancers are relatively rare in less economically developed countries, where malignancies of the upper gastrointestinal tract are quite common. The cancers of the upper gastrointestinal tract have been related to various food practices or preservation methods other than refrigeration. For example, cancer of the mouth and pharynx is the sixth most common cancer world-wide

and has been linked to alcohol consumption, tobacco, salt-preserved meat and fish, smoked foods and charcoal-grilled meat, as well as ingestion of beverages drunk very hot. Thus, diet can be a direct supply of genotoxic compounds or may cause chronic irritation or inflammation (Giovannucci, 1999).

In recent years, many genes involved in the processes described above and other areas of metabolism have been found to exist in allelic form. Therefore, certain populations, subpopulations, races etc have greater or lesser susceptibility to particular diseases linked with variation in alleles of some genes. For many decades, health advice, for example relating to diet, exercise, smoking, sunbathing has been issued by Governments, charities and health advisory bodies, such advice has been directed only at the population as a whole, or, at best, to groups such as the elderly, children and pregnant women. Such advice can therefore only be very general and cannot, by its very nature, take account of the particular genotype of an individual. Moreover, in recent years, there has been much media publicity of research findings on links between particular foods, drugs etc and medical conditions, often causing health scares. As the factors that contribute to disease susceptibility, for example cancer, or cardiovascular disease susceptibility vary between populations and between individuals of populations, it is often impossible for an individual to derive useful advice appropriate to his or her particular circumstances from such reports.

Summary of The Invention

In order to enable individuals to protect and manage their own health, there is a need for individuals to have personally-

tailored information about risk factors which may be important to that individual's well-being and personally- tailored advice on reducing the risk of disease.

Accordingly, the invention provides a computer assisted method of providing a personalized lifestyle advice plan for a human subject comprising:

(i) providing a first dataset on a data processing means, said first dataset comprising information correlating the presence of individual alleles at genetic loci with a lifestyle risk factor, wherein at least one allele of each genetic locus is known to be associated with increased or decreased disease susceptibility;

(ii) providing a second dataset on a data processing means, said second dataset comprising information matching each said risk factor with at least one lifestyle recommendation;

(iii) inputting a third dataset identifying alleles at one or more of the genetic loci of said first dataset of said human subject;

(iv) determining the risk factors associated with said alleles of said human subject using said first dataset;

(v) determining at least one appropriate lifestyle recommendation based on each identified risk factor from step (iv) using said second dataset; and

(vi) generating a personalized lifestyle advice plan based on said lifestyle recommendations.

By lifestyle risk factors, it is meant risk factors associated with dietary factors, exposure to environmental factors, such as smoking, environmental chemicals or sunlight. Similarly lifestyle recommendations should be interpreted as relating to recommendations relating to dietary factors and exposure to environmental factors, such as smoking, environmental chemicals or sunlight. Disease susceptibility should be interpreted to include susceptibility to conditions such as allergies.

Thus, the method allows individualised advice to be generated based on the unique genetic profile of an individual and the susceptibility to disease associated with the profile. By individually assessing the genetic make-up of the client, specific risk factors can be identified and dietary and other health advice tailored to the individual's needs. In a preferred embodiment, the lifestyle advice will include recommended minimum or maximum amounts of foodtypes. (Note that an amount may be 0).

Information concerning the sex and health of the individual and /or of the individual's family may also provide indications that a particular polymorphism or group of polymorphisms associated with a particular condition should be investigated. Such information may therefore be used in selection of polymorphisms to be screened for in the method of the invention.

Such factors may also be used in the determination of appropriate lifestyle recommendations in step (v) of the method. For example, recommendations relating to reducing susceptibility to prostate cancer would not be given to women and recommendations relating to susceptibility to ovarian

cancer would not be given to men. Other factors, such as information regarding the age, alcohol consumption, and existing diet of the client may be incorporated into the determination of appropriate lifestyle recommendations in step (v).

The report comprising the personalised dietary advice may be delivered to the client by any suitable means, for example by letter, facsimile or electronic means, such as e-mail. Alternatively, the report may be posted on a secure Web-page of the service provider with access limited to the client by the use of a unique identifier notified to the client either by conventional or electronic mail. The report can therefore comprise one or more hyperlinks to other documents of the report provider's Web-site or to other Web-sites giving relevant information on the particular polymorphisms identified, disease prevention and/or dietary advice.

As such sites would be able to be updated and new hyperlinks added to the report after the report is initially delivered to the client, the information and advice would be able to be updated at any time, thereby allowing the client to access up-to-date yet personalised health and dietary advice over a prolonged period, without the need for requesting another report.

Preferably, the method will involve assessing a variety of loci in order to give a broad view of susceptibility and possible means of minimising disease risk. Although individual polymorphisms may be considered biomarkers for individual cancer risk, the different biomarkers, when considered together, may also reveal a significant cancer risk. For example, the correlation between CYP1A1 activity and cancer

susceptibility varies, dependent on the presence of specific types of CYP1A1 polymorphism as well as the presence of GSTM1 polymorphisms. An individual with an extremely active CYP1A1 gene, leading to high Phase I P450 activity in combination with a null GSTM1 genotype that lacks the detoxifying Phase II activities has a very high risk of developing cancer (Taningher, 1999).

The presence of a particular polymorphism may be indicative of increased susceptibilty to one disease while being indicative of decreased susceptibility to another disease. For example, one allele of the gene encoding epoxide hydrolase, which catalyses the conversion of toxic PAH metabolites formed by CYP1A1 and CYP1A2 into less toxic and more water-soluble trans-dihydrodiols, has recently been found to be associated with increased risk of aflatoxin-induced liver cancer, but also with decreased risk of ovarian cancer (Pluth, 200; Taningher, 1999).

Therefore, it will be important to assess the risk factors associated with other polymorphisms to give meaningful advice on maintaining optimal health.

Preferred genes for which polymorphisms are identified include genes that encode Phase I metabolism enzymes responsible for detoxification of xenobiotics, genes that encode Phase II metabolism enzymes responsible for further detoxification and excretion of xenobiotics, genes that encode enzymes that combat oxidative stress, genes associated with micronutrient deficiency (for example, deficiency of folate, B12 or B6), genes that encode enzymes responsible for metabolism of alcohol, genes that encode enzymes involved in lipid and/or cholesterol metabolism, genes that encode enzymes involved in

clotting, genes that encode trypsin inhibitors, genes that encode enzymes related to susceptibility to metal toxicity, genes which encode proteins required for normal cellular metabolism and growth and genes which encoded HLA Class 2 molecules.

The method of the invention may include the step of determining the presence of individual alleles at one or more genetic loci of the DNA in a DNA sample of the subject, and constructing the dataset used in step (iii) using results of that determination.

Techniques for determining the presence or absence of individual alleles are known to the skilled person. They may include techniques such as hybridization with allele-specific oligonucleotides (ASO) (Wallace, 1981; Ikuta, 1987; Nickerson, 1990, Varlaan-de Vries, 1986, Saiki, 1989 and Zhang, 1991) allele specific PCR (Newton 1989, Gibbs, 1989), solid-phase minisequencing (Syvanen, 1993), oligonucleotide ligation assay (OLA) (Wu, 1989, Barany, 1991; Abravaya, 1995), 5' fluorogenic nuclease assay (Holland, 1991 & 1992, Lee, 1998) US patents 4,683,202, 4,683,195, 5,723,591 and 5,801,155, or Restriction fragment length polymorphism (RFLP) (Donis-Keller, 1987).

In a preferred embodiment, the genetic loci are assessed via a specialised type of PCR used to detect polymorphisms, commonly referred to as the Taqman® assay, in which hybridisation of a probe comprising a fluorescent reporter molecule, a fluorescent quencher molecule and a minor groove binding chemical to a region of interest is detected by removal of quenching of the fluorescent molecule and detection of resultant fluorescence. Details are given below.

In another embodiment, the genetic loci are assessed via hybridisation with allele-specific oligonucleotides, the allele specific oligonucleotides being preferably arranged as an array of oligonucleotide spots stably associated with the surface of a solid support.

The arrays suitable for use in the method of the invention form a further aspect of the present invention.

In order to assay the sample for the alleles to be identified the fragments of DNA comprising the gene(s) of interest may be amplified to produce a sufficient amount of material to be tested.

The present inventors have designed a number of specific primer sets for amplification of gene regions of interest. Such primers may be used in pairs to isolate a particular region of interest in isolation. Therefore in a further aspect of the invention, there is provided a primer having a sequence selected from SEQ ID NO: 86-99, 104-163. In another aspect, there is provided a primer pair comprising primers having SEQ ID NO:n, where n is an even number from 86 -98 or 104-162 in conjunction with a primer having SEQ ID NO:(n+1).

Preferably, however, the primer sets will be used together with other primer sets to provide multiplexed amplification of a number of regions to allow determination of a number of polymorphisms from the same sample. Therefore in a further aspect of the invention, there is provided a primer set comprising at least 5, more preferably 10, 15 primer pairs selected from SEQ ID NO: 86-121.

Brief Description of the Drawings

Figure 1 shows examples of databases 1 and 2 which may be used in an embodiment of the present invention.

Figure 2 is a flow chart illustrating an embodiment of the invention.

Detailed Description of the Invention

Selection of Genetic Polymorphisms for Datasets

The correct selection of genetic polymorphisms is important to the provision of accurate and meaningful advice. Although not limited to such classes of polymorphisms, in a preferred embodiment of the present invention, markers for polymorphisms of one or more of the following classes of genes are used:

The first dataset of the method of the invention may comprise information relating to two or more alleles of one or more genetic loci of genes selected from the group comprising:
(a) genes that encode enzymes responsible for detoxification of xenobiotics in Phase I metabolism;
(b) genes that encode enzymes responsible for conjugation reactions in Phase II metabolism;
(c) genes that encode enzymes that help cells to combat oxidative stress;
(d) genes associated with micronutrient deficiency;
(e) genes that encode enzymes responsible for metabolism of alcohol.
(f) genes that encode enzymes involved in lipid and/or cholesterol metabolism;
(g) genes that encode enzymes involved in clotting;
(h) genes that encode trypsin inhibitors;

(i) genes that encode enzymes related to susceptibility to metal toxicity;
(j) genes which encode proteins required for normal cellular metabolism and growth;
(k) genes which encoded HLA Class 2 molecules.

The dataset will preferably comprise information relating to two or more alleles of at least two genetic loci of genes selected from the group comprising categories a - k as described above, for example, a+b, a+c, a+d, a+e, a+f, a+g, a+h, a+i, a+j, a+k, b+c, b+d, b+e etc., c+d, c+e etc, d+e, d+f etc, e+f, e+g etc, f+g, f+h etc., g+h, g+i, g+k, h+i, h+k. Where the dataset comprises information relating to two or more alleles of at least two genetic loci, it is preferred that at least one of the genetic loci is of category d, due to the central role of micronutrients in the maintenance of proper cellular growth and DNA repair, and due to the association of micronutrient metabolism or utilisation disorders with several different types of diseases (Ames 1999; Perera, 2000; Potter, 2000). More preferably, the dataset will preferably comprise information relating to two or more alleles of at least three genetic loci selected from the group comprising categories a - k as described above. Where the dataset comprises information relating to alleles of at least three genetic loci, it is preferred that at least two of the genetic loci are of categories d and e. Information relating to polymorphisms present in both of these categories is particularly useful due to the effects of alcohol consumption and metabolism on the efficiency of enzymes related to micronutrient metabolism and utilisation (Ulrich, 1999). In a further preferred embodiment, where the dataset comprises information relating to alleles of at least three genetic loci, it is preferred that at least two of the genetic loci

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are of categories a and b due to the close interaction of Phase I and Phase II enzymes in the metabolism of xenobiotics. Even more preferably, the dataset will comprise information relating to two or more alleles of at least four genetic loci of genes selected from the group comprising categories a - k as defined above, for example, a+b+c+d, a+b+c+e, a+b+d+e, a+c+d+e, b+c+d+e etc. Where the dataset comprises information relating to alleles of at least four genetic loci, it is preferred that at least three of the genetic loci are of categories d and e and f Information relating to polymorphisms present in these three categories is particularly useful due to the strong correlation of polymorphisms of these alleles with coronary artery disease due to the combined effects of altered micronutrient utilisation, affected adversely by alcohol metabolism, together with imbalances in fat and cholesterol metabolism. Further, where the dataset comprises information relating to alleles of at least five genetic loci, it is preferred that at least four of the genetic loci are of categories a, b, d and e. Information relating to polymorphisms present in these four categories is particularly useful due to the combined effects of micronutrients utilisation, alcohol metabolism, Phase 1 metabolism of xenobiotics and Phase II metabolism on the further metabolism and excretion of potentially harmful metabolites produced in the body (Taningher, 1999; Ulrich, 1999). Similarly, the dataset may comprise information relating to two or more alleles of at least five, for example a, b, d, e and f, six, seven, eight, nine or ten genetic loci of genes selected from the group comprising categories a - k as defined above.

Preferably, the dataset will comprise information relating to two or more alleles of one or more genetic loci of genes

selected from each member of the group comprising categories a - k as described above. In a preferred embodiment, the first dataset comprises information relating to two or more alleles of the genetic loci of genes encoding each of the cytochrome P450 monooxygenase, N-acetyltransferase 1, N-acetyltransferase 2, glutathione-S-transferase, manganese superoxide dismutase, 5,10-methylenetetrahydrofolatereductase and alcohol dehydrogenase 2 enzymes. In a more preferred embodiment the first dataset further comprises information relating to two or more alleles of the genetic loci of genes encoding one or more, preferably each of epoxide hydrolase (EH), NADPH-quinone reductase (NQ01), paraxonaoase (PON1), myeloperoxidase (MPO), alcohol dehydrogenase 1, alcohol dehydrogenase 3, cholesteryl ester transfer protein, apolipoprotein A IV, apolipoprotein E, apolipoprotein C III, angiotensin, factor VII, prothrombin 20210, β-fibrinogen, heme -oxygenase-1, α-antitrypsin, SPINK1, Δ-aminolevulinacid dehydratase, interleukin 1, interleukin 1, vitamin D receptor, B1 kinin receptor, cystathionine-beta-synthase, methionine synthase (B12 MS), 5-HT transporter, transforming growth factor beta 1 (TGFβ1), L-myc, HLA Class 2 molecules, T-lymphocyte associated antigen 4 (CTLA-4), interleukin 4, interleukin 3, interleukin 6, IgA, and/or galactose metabolism gene GALT.

<u>Genes that encode enzymes responsible for (a)detoxification of xenobiotics in Phase I metabolism; and(b) conjugation reactions in Phase II metabolism</u>.

Xenobiotics are potentially toxic compounds found in, for example, char-grilled red meat. Meat consumption is associated with increased risk of cancer, especially well-done meat cooked at high temperatures (Sinha, 1999). Cooking meat in this fashion leads to the production of heterocyclic amines

(HCA), nitrosamines (NA), and polycyclic aromatic hydrocarbons (PAH), which have known carcinogenic activity in animals (Hirvonen, 1999; Layton, 1995).

Detoxification of xenobiotics occurs in 2 phases in humans:

Phase I metabolism involves the addition of an oxygen atom or a nitrogen atom to lipophilic (fat soluble) compounds, such as steroids, fatty acids, xenobiotics (from external sources like diet, smoke, etc.) so that they can be conjugated by the Phase II enzymes (thus made water-soluble) and excreted from the body (Hirvonen, 1999). Individuals with genetic polymorphisms correlated with cancer risk in these genes should avoid consumption of char-grilled foods, smoked fish, well-done red meat whether grilled or pan-fried (Sinha, 1999). They should also increase consumption of food products known to increase Phase II metabolism so the products of Phase I metabolism may be cleared more efficiently.

Specific examples of genes of category a for which information relating to polymorphisms may be used in the present invention include genes encoding cytochrome P450 monooxygenase (CYP) e.g. CYP1A1, CYA1A2, CYP2C, CYP2D6, CYP2E1, CYP3A4, CYP11B2, genes encoding N-acetyltransferase 1 e.g. NAT1, genes encoding N-acetyltransferase 2 e.g. NAT2, genes encoding epoxide hydrolase (EH), genes encoding NADPH-quinone reductase (NQ01, genes encoding paraxonaoase (PON1), genes encoding myeloperoxidase (MPO).

CYP is also referred to as cytochromome P450 monooxygenase (gene is called CYP, enzyme is called P450). P450 enzymes belong to a super-family with wide substrate activity that catalyses the insertion of an oxygen atom into a substrate.

The reaction can convert a molecule (procarcinogen) into a DNA-reactive electrophilic carcinogen (Hirvonen, 1999; Smith, 1995). Polymorphisms in genes encoding cytochrome P450 (CYP family of genes) are associated with altered susceptibility to cancer, CAD and altered metabolisim of various pharmaceutical agents (Poolsup, 2000; Miki, 1999; Cramer,2000; Marchand, 1999; Sinha, 1997).

CYP1A1 codes for a P450 enzyme that metabolises polycyclic aromatic hydrocarbons (PAH). The CYP1A1 gene is polymorphic and is inducible by PAH, which means that expression of the enzyme is increased upon exposure to PAH (MacLeod, 1997). CYP1A1 is located on chromosome 15q22-q24 (Smith, 1995). This gene has been linked to colorectal, urinary bladder, breast, oral cavity, stomach, and lung cancers (Perera, 2000; Garte, 1998). The gene product, the P450 enzyme, is inducible by exposure to the agents that it metabolises, so the consumption of high levels of a potential source of carcinogens, such as well-done red meat, would increase the production of the enzyme and thus the creation of carcinogenic substances (Mooney, 1996; Perera, 2000; Alexandrie, A.K., 2000). Studies of polymorphisms of the CYP1A1 gene have revealed considerable differences in enzyme activity, with corresponding differences in cancer risk after exposure to known substrates of the enzyme (Alexandrie, 2000; Rojas, 2000; Garte, 2000). Both the Ile-Val polymorphism I, which comprises an A4889G substitution (i.e. the adenine residue at position 4889 of the 5′ – 3′ strand is substituted by a guanine residue) and the CYP1A1*C polymorphism, which comprises an T6235C substitution, are induced to a greater extent than the wild type gene after exposure to PAH, and have been associated with a significant increase in cancer risk (Taningher, 1999; Garte, 1998; Kawajiri, 1996; MacLeod, S., 1997; Smith, 1995).

Approximately 10 percent of the Caucasian population carries polymorphisms linked to cancer risk, according to a recent American review paper (Shields, 2000). Polymorphisms in genes encoding CYP1A2, CYP2C, CYP2D6, CYP2E1, CYP3A4, CYP11B2 are associated with altered susceptibility to cancer and drug sensitivity. (Poolsup, 2000; Miki, 1999; Cramer,2000; Marchand, 1999; Sinha, 1997).

NAT1 (N-acetyltransferase 1) and NAT2 (N-acetyltransferase 2) also activate PAH and heterocyclic amines (HAA). The enzymes catalyse N-acetylation, O-acetylation, and N,O-acetylation. The O-acetylation reaction is considered the most risky, with the potential for forming chemical carcinogens that can bind to DNA. The N-acetylation reaction can occur on a compound after a P450 has inserted an oxygen, thus increasing the water solubility of the compound so it may be excreted. Due to this activity, the NAT genes are often considered as both Phase I and Phase II type enzymes. The literature describing a cancer link focuses on the activation activity of the enzymes, so they will be listed in the Phase I section only. There are 3 separate N-acetyltransferase genes in humans, two are active genes: NAT1 and NAT2, and a pseudogene, NATP. Pseudogenes have the same sequence, but lack apparent function and promoter elements and are not expressed in cells (i.e. the gene is not transcribed into RNA then translated into amino acids to make a protein/enzyme) (Perera, 2000). NAT1 and NAT2 genes are located on chromosome 8 at 8p21.3-21.1, both genes are 870 bp long and both code for a protein 290 amino acids in length. The genes are highly polymorphic and epidemiological studies have sometimes given conflicting information regarding links with cancer. The genes show geographical and ethnic variation and the enzyme activity varies considerably within different tissues or organs. There are approximately 20

polymorphisms for NAT1 known to date, but the list below only includes the polymorphisms that have shown a link to cancer (Hein, 2000a). The current list of nomenclature and polymorphisms is kept at a web site: http://www.louisville.edu/medschool/pharmacology/NAT.html.

Many of the epidemiological studies of both NAT1 and NAT2 used phenotyping assays, which measured enzyme activity, and found fast and slow acetylator types, with the fast phenotype carrying an increased risk for cancer in the colon (Perera, 2000). However, later analysis of the results found that the fast/slow phenotype could vary considerably depending on the substrate chosen for acetylation (Hein, 2000a). Recent studies have used genetic sequence data to more precisely match acetylator activity and cancer risk with polymorphism (Hein, 2000b). Although the genes are the same size, they do act on different substrates. For example, caffeine is a substrate for NAT2 but not for NAT1.

NAT1 is expressed to a higher degree than NAT2 in the colon, so NAT1 may be associated with localised activity of activated HAA or PAH in the colon (Brockton, 2000; Perera, 2000). The polymorphism NAT1*10,, which comprises T1088A and C1095A substitutions, and which has a fast phenotype, has been consistently linked with an increased risk of colon cancer and higher DNA adduct levels (i.e. DNA damage that can lead to cancer) in colon tissue (Perera, 2000; Ilett, 1987). The NAT1*11 polymorphism has been linked to risk of breast cancer in women who smoke or consume well-done red meat (Zheng, 1999). However, the phenotype is not well understood, so this marker cannot be categorized as a fast or slow acetylator (Doll, 1997). Two alleles of the NAT1*11 polymorphism are known: the NAT1*11A polymorphism, which comprises C(-344)T,

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A(-40)T, G445A, G459A, T640G, C1095A substitutions and a Δ9:1065-1090 deletion; and the NAT1*11B polymorphism, which comprises C(-344)T, A(-40)T, G445A, G459A, T640G substitutions and a Δ9:1065-1090 deletion. References to NAT1*11 polymorphisms should be understood to include reference to NAT1*11A or NAT1*11B polymorphisms.

NAT1*14 on the other hand has little or no enzyme activity (Brockton, 2000) and has been associated with increased lung cancer risk (Bouchardy, C., 1998). Two alleles of the NAT1*14 polymorphism are known: the NAT1*14A polymorphism, which comprises G560A, T1088A and C1095A substitutions; and the NAT1*14B polymorphism, which comprises a G560A substitution. References to NAT1*14 polymorphisms should, except where the context dictates otherwise, be understood to include reference to NAT1*14A or NAT1*14B polymorphisms. The NAT1*14 polymorphism shares a restriction enzyme site with the NAT1*11polymorphism, and some of the conflicting results reported in the literature are believed to be due to the inability of the assay used (restriction fragment length polymorphism assay (RFLP)) to distinguish the polymorphisms (Hein, 2000a). The oligonucleotide array suitable for use in the present invention can distinguish all polymorphisms and therefore will be more precise than the RFLP procedure.

NAT2 is expressed primarily in the liver, but has been linked with cancer incidence in other organs (Hein, 2000b). NAT2*5A, which comprises T481C and T341C substitutions, NAT2*6A, which comprises C282T and G590A substitutions, NAT2*7A, which comprises a G857A substitution, have reduced acetylation activity (Hein, 2000b) and have been linked to risk of bladder cancer (Taningher, 1999; Lee, 1998). NAT2*4, is considered the normal, or wild type, sequence. NAT2*4 has fast

acetylator activity and has been linked to increased cancer risk in several studies (reviewed in Hein, 2000b; Gil, 1998), but especially in conjunction with the NAT1*10 polymorphism (Bell, 1995). NAT2 rapid/intermediate acetylators with at least one NAT2*4 allele have been linked to breast cancer in women who consumed well-done red meat (Dietz, 1999). Approximately 55% of the Caucasian population carry NAT1 polymorphisms linked to cancer. (Shields, 2000).

Polymorphisms in genes encoding epoxide hydrolase are associated with cancer and chronic obstructive pulmonary disease (Pluth, 200; Miki,1999). Polymorphisms in genes encoding NADPH-quinone reductase are associated with altered susceptibility to cancer (Nakajima, 2000). Polymorphisms in genes encoding paraxonoase are associated with altered susceptibility to cancer and to CAD (MacKness, 2000). Polymorphisms in genes encoding myeloperoxidase are associated with altered susceptibility to CAD (Schabath, 2000).

Specific examples of genes of category b for which information relating to polymorphisms may be used in the present invention include genes encoding glutathione-S-transferase e.g GSTM1, GSTP1, GSTT1.

Glutathione-S-transferases catalyse the reaction of electrophilic compounds with glutathione so the compounds may be excreted from the body. The enzymes belong to a super-family with broad and overlapping substrate specificities. Glutathione-S-transferases provide a major pathway of protection against chemical toxins and carcinogens and are thought to have evolved as an adaptive response to environmental insult, thus accounting for their wide substrate specificity (Hirvonen, 1999). There are 4 family members:

alpha, mu, theta, and pi, also designated as A, M, T and P. Polymorphisms have been identified in each family (Perera, 2000). Individuals with low glutathione-S-transferase activity should avoid meats cooked at higher temperatures as above, and increase fruit and vegetable consumption. Cruciferous vegetables such as broccoli and members of the allium family such as garlic and onion have been shown to be potent inducers of these enzymes, which would be expected to increase clearance of toxic substances from the body (Cotton, 2000; Giovannucci, 1999).

GSTmu, has 3 alleles: null, a,, which is considered to be the wild type, and b, which comprises a C534G substitution, with no functional difference between the a and b alleles. The GSTmu sub-type has the highest activity of the 4 types and is predominately located in the liver (Hirvonen, 1999). Approximately half of the population has a complete deletion of this gene with a corresponding risk of lung, bladder, breast, liver, and oral cavity cancer (Shields, 2000; Perera, 2000). It has been estimated that 17% of all lung and bladder cancers may be attributable to GSTM1 null genotypes (Hirvonen, 1999). GSTM1 null genotype together with a highly active CYP1A1 polymorphism has been linked to a very high cancer risk in several studies (Rojas, 2000; Shields, 2000). The GSTM1 gene is located on chromosome 1p13.3 (Cotton, 2000).

GSTpi gene is located on chromosome 11q13. This sub-type is known to metabolise many carcinogenic compounds and is the most abundant sub-type in the lungs (Hirvonen, 1999). Two single nucleotide polymorphisms have been linked to cancer to date GSTP1*B, which comprises an A313G substitution, and GSTP1*C, which comprises a C341T substitution. The enzymes of these polymorphic genes have decreased activity compared to

the wild type and a corresponding increased risk of bladder, testicular, larynx and lung cancer (Harries, 1997; Matthias, 1998; Ryberg, 1997).

GSTtheta gene is on chromosome 22q11.2 and is deleted in approximately 20% of the Caucasian population. The enzyme is found in a variety of tissues, including red blood cells, liver, and lung (Potter, 1999). The deletion is associated with an increased risk of lung, larynx and bladder cancers (Hirvonen, 1999). Links with GSTM1 null genotypes are currently being searched, as it is believed that individuals that have both GSTM1 and GSTT1 alleles deleted will have a greatly increased risk of developing cancer (Potter, 1999).

Genes that code for enzymes that help cells to combat oxidative stress

Specific examples of genes of category c for which information relating to polymorphisms may be used in the present invention include genes encoding manganese superoxide dismutase (MnSOD or SOD2 gene).

Manganese superoxide dismutase is an enzyme that destroys free radicals or a free-radical scavenger. The gene is located on chromosome 6q25.3, but the enzyme is found within the mitochondria of cells. There are 2 polymorphisms linked to cancer to date, an Ile 58Thr allele, which comprises an T175C substitution, and a Val(-9)Ala allele, which comprises a T(-28)C substitution,. A study of premenopausal women found a four-fold increased risk of breast cancer in individuals with the Val(-9)Ala polymorphism and the highest risk within this group is found in women who consumed low amounts of fruits and vegetables (Ambrosone, 1999). This polymorphism occurs in the

signal sequence of the amino acid chain. The signal sequence ensures transport of the enzyme into the mitochondria of the cell, and so the polymorphism is believed to reduce the amount of enzyme delivered to the mitochondria (Ambrosone, 1999). The mitochondria is commonly referred to as the workhorse of the cell, where the energy-yielding reactions take place. This is the site of many oxidative reactions, so many free radicals are generated here. Individuals with low activity of this enzyme should be advised to take antioxidant supplements and increase consumption of fruits and vegetables (Giovannucci, 1999; Perera, 2000).

Genes associated with Micronutrient deficiency e.g. of folate, vitamin B12 or vitamin B6

Specific examples of genes of category d for which information relating to polymorphisms may be used in the present invention include the gene encoding 5,10-methylenetetrahydrofolatereductase (MTHFR) activity.

5,10-methylenetetrahydrofolate reductase is active in the folate-dependent methylation of DNA precursors. Low activity of this enzyme leads to an increase of uracil incorporation into DNA (instead of thymine) (Ames, 1999). The MTHFR gene is polymorphic and has been linked to colon cancer, adult acute lymphocytic leukaemia and infant leukaemia (Ames, 1999; Perera, 2000; Potter, 2000). Both the wt and polymorphic alleles have been linked to disease, each being dependent on levels of folate in the diet. Approximately 35% of the Caucasian population has genetic polymorphisms at this locus with corresponding risk of colon cancer (Shields, 2000). Polymorphisms at this locus include those with a C677T or A1298C substitution. Dietary recommendations for individuals

lacking in MTHFR activity include taking supplements with folate and increasing consumption of fruit and vegetables (Ames, 1999). Low levels of vitamins B12 and B6 have been associated with low MTHFR activity and increased cancer risk, so individuals should increase intake of these vitamins; B12 is found primarily in meat and B6 is found in whole grains, cereals, bananas, and liver (Ames, 1999). Alcohol has a deleterious effect on folate metabolism, affecting individuals with the A1298C polymorphism most severely (Ulrich, 1999). These individuals should be advised to avoid alcohol.

Genes that code for enzymes responsible for metabolism of alcohol

Specific examples of genes of category e for which information relating to polymorphisms may be used in the present invention include genes encoding alcohol dehydrogenase e.g. the ALDH2 gene, ALDH1 gene and ALDH3 gene.

Alcohol dehydrogenase 2 (ALDH2) is involved in the second step of ethanol utilisation. Reduced activity of this enzyme leads to accumulation of acetaldehyde, a potent DNA adduct former (Bosron, 1986). There has been one polymorphism identified to date, the ALDH2*2 polymorphism, which comprises a G1156A substitution, and which has links with oesophageal/throat cancer, stomach, lung, and colon cancer (IARC, 1998; Yokoyama, 1998). The advice to individuals with the polymorphism would be to avoid alcohol. Polymorphisms in ALDH1 and 3 are associated with increased susceptibility to cancers and Parkinson's disease.

Genes that encode enzymes involved in lipid and/or cholesterol metabolism

Specific examples of genes of category f for which information relating to polymorphisms may be used in the present invention include genes encoding cholesteryl ester transfer protein e.g. the CETP gene, polymorphisms of which genes are associated with altered susceptibility to coronary artery disease (CAD)((Raknew, 2000; Ordovas, 2000); genes encoding apolipoprotein A, IV (ApoA-IV), polymorphisms of which genes are associated with altered susceptibility to coronary artery disease (CAD) (Wallace,2000; Heilbronn, 2000); apolipoprotein E(ApoE), polymorphisms of which genes are associated with altered susceptibility to CAD and Alzheimer's disease (Corbo,1999; Bullido, 2000); or apolipoprotein C, III (ApoC-III), polymorphisms of which genes are associated with altered susceptibility to CAD, hypertension and insulin resistance (Salas, 1998).

Genes that encode enzymes involved in clotting mechanisms

Specific examples of genes of category g for which information relating to polymorphisms may be used in the present invention include genes encoding angiotensin (AGT-1) and angiotensin converting enzyme (ACE), polymorphisms of which genes are associated with altered susceptibility to hypertension (Brand 2000;de Padua Mansur, 2000), factor VII, polymorphisms of which genes are associated with altered susceptibility to CAD (Donati, 2000; Di Castelnuovo, 2000); prothrombin 20210, polymorphisms of which genes are associated with altered susceptibility to venous thrombosis (Vicente, 1999); β-fibrinogen, polymorphisms of which genes are associated with altered susceptibility to CAD (Humphries, 1999); or heme - oxygenase-1, polymorphisms of which genes are associated with altered susceptibility to emphysema (Yamada, 2000).

Genes that encode trypsin inhibitors

Specific examples of genes of category h for which information relating to polymorphisms may be used in the present invention include genes encoding α-antitrypsin, polymorphisms of which genes are associated with altered susceptibility to chronic obstructive pulmonary disease (COPD) (Miki, 1999); or serine protease inhibitor, Kazal type 1(SPINK), polymorphisms of which genes are associated with altered susceptibility to pancreatitis (Pfutzer, 2000).

Genes that encode enzymes related to susceptibility to metal toxicity

Specific examples of genes of category i for which information relating to polymorphisms may be used in the present invention include genes encoding Δ-aminolevulinacid dehydratase, polymorphisms of which genes are associated with altered susceptibility to lead toxicity (Costa, 2000).

Genes which encode proteins required for normal cellular metabolism and growth

Specific examples of genes of category j for which information relating to polymorphisms may be used in the present invention include genes encoding the vitamin D receptor, polymorphisms of which genes are associated with altered susceptibility to osteoporosis, tuberculosis, Graves disease, COPD, and early periodontal disease (Ban, 2000; Wilkinson, 2000; Gelder, 2000; Miki, 1999; Hennig, 1999); the B1 kinin receptor (B1R), polymorphisms of which genes are associated with altered susceptibility to kidney disease (Zychma, 1999);

cystathionine-beta-synthase, polymorphisms of which genes are associated with altered susceptibility to CAD (Tsai, 1999); methionine synthase (B12 MS), polymorphisms of which genes are associated with altered susceptibility to CAD (Tsai, 1999); the 5-HT transporter, polymorphisms of which genes are associated with altered susceptibility to neurological disorders, Alzheimer's disease, schizophrenia, other disorders of the serotonin pathway (Oliveira, 1999); tumour necrosis factor receptor 2 (TNFR2), polymorphisms of which genes are associated with altered susceptibility to CAD (Fernandez-Real, 2000); galactose metabolism gene GALT, polymorphisms of which genes are associated with altered susceptibility to ovarian cancer (Cramer, 2000); transforming growth factor beta 1 (TGFβ1), polymorphisms of which genes are associated with altered susceptibility to CAD and cancers (Yokota, 2000); and L-myc, polymorphisms of which genes are associated with altered susceptibility to CAD (especially in relation to tolerance to smoking) and cancers (Togo, 2000).

<u>Genes which encoded proteins associate with immunological susceptibility</u>

Specific examples of genes of category k for which information relating to polymorphisms may be used in the present invention include genes encoding HLA Class 2 molecules, polymorphisms of which genes are associated with altered susceptibility to cervical cancer and human papilloma virus (HPV) infection (Maciag, 2000); T-lymphocyte associated antigen 4 (CTLA-4), polymorphisms of which genes are associated with altered susceptibility to liver disease (Argawal, 2000); interleukin 1 (IL-1), polymorphisms of which are associated with cardiovascular disease and periodontal disease (macaiag, 2000; Nakajima, 2000); IL-4, polymorphisms of which genes are

associated with altered susceptibility to atopy and asthma (Rosa-Rosa, 1999); IL-3, polymorphisms of which genes are associated with altered susceptibility to atopy and asthma (Rosa-Rosa, 1999); IL-6, polymorphisms of which genes are associated with altered susceptibility to osteoporosis; and IgA, polymorphisms of which genes are associated with altered susceptibility to COPD (Miki, 1999).

<u>Detection of Polymorphisms</u>

As described above, the method of the invention may include the step of analysing a DNA sample of a human subject in order to construct the dataset to be used in the method of the invention.

<u>Testing of Samples</u>

<u>Collection of Tissue Samples</u>

DNA for analysis using the method or arrays of the invention can be isolated from any suitable client or patient cell sample. For convenience, it is preferred that the DNA is isolated from cheek (buccal) cells. This enables easy and painless collection of cells by the client, with the convenience of being able to post the sample to the provider of the genetic test without the problems associated with posting a liquid sample.

Cells may be isolated from the inside of the mouth using a disposable scraping device with a plastic or paper matrix "brush", for example, the C.E.P. Swab™ (Life Technologies Ltd., UK). Cells are deposited onto the matrix upon gentle abrasion of the inner cheek, resulting in the collection of

approximately 2000 cells (Aron, 1994). The paper brush can then be left to dry completely, ejected from the handle placed into a microcentrifuge tube and posted by the client or patient to the provider of the genetic test.

Isolation of DNA from Samples

DNA from the cell samples can be isolated using conventional procedures. For example DNA may be immobilised onto filters, column matrices, or magnetic beads. Numerous commercial kits, such as the Qiagen QIAamp kit (Quiagen, Crawley, UK) may be used. Briefly, the cell sample may be placed in a microcentrifuge tube and combined with Proteinase K, mixed, and allowed to incubate to lyse the cells. Ethanol is then added and the lysate is transferred to a QIAamp spin column from which DNA is eluted after several washings.

The amount of DNA isolated by the particular method used may be quantified to ensure that sufficient DNA is available for the assay and to determine the dilution required to achieve the desired concentration of DNA for PCR amplification. For example, the desired target DNA concentration may be in the range 10 ng and 50 ng. DNA concentrations outside this range may impact the PCR amplification of the individual alleles and thus impact the sensitivity and selectivity of the polymorphism determination step.

The quantity of DNA obtained from a sample may be determined using any suitable technique. Such techniques are well known to persons skilled in the art and include UV (Maniatis, 1982) or fluorescence based methods. As UV methods may suffer from the interfering absorbance caused by contaminating molecules such as nucleotides, RNA, EDTA and phenol and the dynamic

range and sensitivity of this technique is not as great as that of fluorescent methods, fluorescence methods are preferred. Commercially available fluorescence based kits such as the PicoGreen dsDNA Quantification (Molecular Probes, Eugene, Oregon, USA).

Primers

Prior to the testing of a sample, the nucleic acids in the sample may be selectively amplified, for example using Polymerase Chain Reaction (PCR) amplification. as described in U.S. patent numbers 4,683,202 AND 4,683,195.

Preferred primers for use in the present invention are from 18 to 23 nucleotides in length, without internal homology or primer-primer homology.

Furthermore, to ensure amplification of the region of interest and specificity, the two primers of a pair are preferably selected to hybridise to either side of the region of interest so that about 150 bases in length are amplified, although amplification of shorter and longer fragments may also be used. Ideally, the site of polymorphism should be at or near the centre of the region amplified.

Table 1 provides preferred examples of primer pairs which may be used in the invention, particularly when the Taqman® assay is used in the method of the invention. The primers are shown together with the gene targets and preferred examples of the wt probes and polymorphism probes used in the Taqman® assay for each gene target.

Table 2 provides preferred examples of the primer pairs which

may be used in the invention together with the gene targets and the size of the fragment isolated using the primers, which they amplify.

The primers and primer pairs form a further aspect of the invention. Therefore the invention provides a primer having a sequence selected from SEQ ID NO: 86-99, 104-163. In another aspect, there is provided a primer pair comprising primers having SEQ ID NO:n, where n is an even number from 86 -98 or 104-162 in conjunction with a primer having SEQ ID NO:(n+1).

In a preferred embodiment of the invention, multiplexed amplification of a number of sequences are envisioned in order to allow determination of the presence of a plurality of polymorphisms using, for example the DNA array method. Therefore, primer pairs to be used in the same reaction are preferably selected by position, similarity of melting temperature, internal stability, absence of internal homology or homology to each other to prevent self-hybridisation or hybridisation with other primers and lack of propensity of each primer to form a stable hairpin loop structure. Thus, the sets of primer pairs to be coamplified together preferably have approximately the same thermal profile, so that they can be effectively coamplified together. This may be achieved by having groups of primer pairs with approximately the same length and the same G/C content.

Therefore in a further aspect of the invention, there is provided a primer set comprising at least 5, more preferably 10, 15 primer pairs selected from SEQ ID NO: 86-121.

Table 1

Gene	Forward primer	Reverse primer	WT Probe	Polymorphism probe
1. CYP1A1				
A4889G	CATGGGCAAGCG GAAGTG (SEQ ID NO:122)	CAGGATAGCCAGGAA GAGAAAGAC (SEQ ID NO:123)	CGGTGAGACCaTTG (SEQ ID NO:164)	CGGTGAGACCgTTG (SEQ ID NO:165)
T6235C	AGACAGGGTCCCCAGG TCAT (SEQ ID NO:124)	CAGAGGCTGAGGTGG GAGAA (SEQ ID NO:125)	CTCCACCTCCtGGG (SEQ ID NO:166)	CTCCACCTCCcGGG (SEQ ID NO:167)
2. NAT1				
G445A	GGAGTTAATTTCTGGG AAGGATCAG (SEQ ID NO:126)	TGGTCTAGATACCAG AATCCATTCTCTT (SEQ ID NO:127)	GCCTTGTgTCTTC (SEQ ID NO:168)	TGCCTTGTaTCTTC (SEQ ID NO:169)
G459A	GGCAGCCTCTGGAGTT AATTTCT (SEQ ID NO:128)	TTCCCTTCTGATTTG GTCTAGATACC (SEQ ID NO:129)	CGTTTGACgGAAGAG (SEQ ID NO:170)	CGTTTGACaGAAGAG (SEQ ID NO:171)
G560A	GGGAACAGTACATTCC AAATGAAGA (SEQ ID NO:130)	TGTTCGAGGCTTAAG AGTAAAGGAGT (SEQ ID NO:131)	AATACCgAAAAATC (SEQ ID NO:172)	CAAATACCaAAAAAT (SEQ ID NO:173)
T640G	AACAATTGAAGATTTT GAGTCTATGAATACA (SEQ ID NO:132)	TCTGCAAGGAACAAA ATGATTTACTAGT (SEQ ID NO:133)	CATCTCCAtCATCTG (SEQ ID NO:174)	ACATCTCCAgCATCT (SEQ ID NO:175)
T1088A	GAAACATAACCA CAAACCTTTTCA AA (SEQ ID NO:134)	AAATCACCAATTTCC AAGATAACCA (SEQ ID NO:135)	CCATCTTTAAAATACA TTTaTTA (SEQ ID NO:203)	CATCTTTAAAATACA TTTtTTA (SEQ ID NO:204)
C1095A	AAACATAACCAC AAACCTTTTCAA ATAAT (SEQ ID NO:136)	AAATCACCAATTTCC AAGATAACCA (SEQ ID NO:137)	GCCATCTTTAAAAgAC AT (SEQ ID NO:176)	GCCATCTTTAAAAtA CATT (SEQ ID NO:177)
3. NAT2				
C>T	AATCAACTTCTGTACT GGGCTCTGA	CCATGCCAGTGCTGT ATTTGTT	AGGGTATTTTTAcATC CCT	AGGGTATTTTTAtAT CCCTC

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Gene	Forward primer	Reverse primer	WT Probe	Polymorphism probe
	(SEQ ID NO:138)	(SEQ ID NO:139)	(SEQ ID NO:178)	(SEQ ID NO:179)
C>T2	TGCATTTTCTGCTTGA CAGAAGA (SEQ ID NO:140)	TTTGTTTGTAATATA CTGCTCTCTCCTGAT (SEQ ID NO:141)	TCTGGTACCTGGACCA A (SEQ ID NO:180)	AATCTGGTACtTGGA CCAA (SEQ ID NO:181)
G>A	GCCAAAGAAGAAACAC CAAAAAAT (SEQ ID NO:142)	AAATGATGTGGTTAT AAATGAAGATGTTG (SEQ ID NO:143)	TGAACCTCgAACAAT (SEQ ID NO:182)	TTGAACCTCaAACAA TT (SEQ ID NO:183)
G>A2	AAGAGGTTGAAGAAGT GCTGAAAAAATAT (SEQ ID NO:144)	ATACATACACAAGGG TTTATTTTGTTCCT (SEQ ID NO:145)	CTGGTGATGgATCC (SEQ ID NO:184)	CTGGTGATGaATCC (SEQ ID NO:185)
4. GSTM1				
C534G	GTTCCAGCCCACACAT TCTTG (SEQ ID NO:146)	CGGGAGATGAAGTCC TTCAGATT (SEQ ID NO:147)	CAAGCAgTTGGGC (SEQ ID NO:186)	CAAGCAcTTGGGC (SEQ ID NO:187)
5. GSTP1				
A313G	CCTGGTGGACATGGTG AATG (SEQ ID NO:148)	GCAGATGCTCACATA GTTGGTGTAG (SEQ ID NO:149)	GCAAATACaTCTCCCT (SEQ ID NO:188)	GCAAATACgTCTCCC T (SEQ ID NO:189)
C341T	GGGATGAGAGTAGGAT GATACATGGT (SEQ ID NO:150)	GGGTCTCAAAAGGCT TCAGTTG (SEQ ID NO:151)	CCTTGCCCgCCTC (SEQ ID NO:190)	CTTGCCCaCCTCC (SEQ ID NO:191)
6. GSTT1	TCATTCTGAAGGCCAA GGACTT (SEQ ID NO:152)	CAGGGCATCAGCTTC TGCTT (SEQ ID NO:153)	CCTGCAGACCCC (SEQ ID NO:192)	N/A
7. MnSOD				
T-28C	GGCTGTGCTTTCTCGT CTTCA (SEQ ID NO:154)	TTCTGCCTGGAGCCC AGAT (SEQ ID NO:155)	ACCCCAAAaCCGGA (SEQ ID NO:193)	ACCCCAAAgCCGGA (SEQ ID NO:194)
T175C	GTGTTGCATTTACTTC AGGAGATGTT (SEQ ID NO:156)	TCCAGAAAATGCTAT GATTGATATGAC (SEQ ID NO:157)	AGCCCAGAtAGCT (SEQ ID NO:195)	AGCCCAGAcAGCT (SEQ ID NO:196)
8. MTHFR				

Gene	Forward primer	Reverse primer	WT Probe	Polymorphism probe
C677T	GACCTGAAGCACTTGA AGGAGAA (SEQ ID NO:158)	TCAAAGAAAAGCTGC GTGATGA (SEQ ID NO:159)	AAATCGgCTCCCGC (SEQ ID NO:197)	AAATCGaCTCCCGCA GA (SEQ ID NO:198)
A1298C	AAGAGCAAGTCCCCCA AGGA (SEQ ID NO:160)	CTTTGTGACCATTCC GGTTTG (SEQ ID NO:161)	CAGTGAAGaAAGTGTC (SEQ ID NO:199)	AGTGAAGcAAGTGTC (SEQ ID NO:200)
9. ALDH2				
G1156A	CCCTTTGGTGGCTACA AGATGT (SEQ ID NO:162)	AGACCCTCAAGCCCC AACA (SEQ ID NO:163)	TCACAGTTTTCACTTc AGTGT (SEQ ID NO:201)	TCACAGTTTTCACTT tAGTGT (SEQ ID NO:202)

Table 2: Examples of Primer pairs

Gene	Primer Set	Forward	Reverse	Size
NAT1	1	N/A same genotype as set 3		
	2	N/A same genotype as set 3		
	3	5'ggg ttt gga cgc tca tac c(SEQ ID NO: 86)	5'aat gta ctg ttc cct tct gat ttg g(SEQ ID NO: 87)	141bp
	4b	5'tcc gtt tga cgg aag aga at (SEQ ID NO: 88)	5'ggg tct gca agg aac aaa at (SEQ ID NO: 89)	234bp
	5	5'gaa aca taa cca caa acc (SEQ ID NO: 90)	5'caa caa taa acc aac att aaa agc (SEQ ID NO: 91)	241bp
NAT2	1	5'act tct gta ctg ggc tct gac c (SEQ ID NO: 92)	5'gca tcg aca atg taa ttc ctg c (SEQ ID NO: 93)	150bp
	2	5'aat aca gca ctg gca tgg (SEQ ID NO: 94)	5'caa gga aca aaa tga tgt gg (SEQ ID NO: 95)	380bp
	3	5'gtg ggc ttc atc ctc acc ta (SEQ ID NO: 96)	5' ggg tga tac ata cac aag ggt tt (SEQ ID NO: 97)	209bp

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Gene	Primer Set	Forward	Reverse	Size
GSTM1	1	5'cag ccc aca cat tct tgg (SEQ ID NO: 98)	5'aag cgg gag atg aag tcc (SEQ ID NO: 99)	196bp
MTHFR	1	5'agg tta ccc caa agg cca cc (SEQ ID NO: 100)	5'gca agt gat gcc cat gtc g (SEQ ID NO: 101)	166bp
	2	5'tct tct acc tga aga gca agt cc (SEQ ID NO: 102)	5'caa gtc act ttg tga cca ttc c (SEQ ID NO: 103)	142bp
CYP1A1	1b	5'cct gaa ctg cca ctt cag c (SEQ ID NO: 104)	5'cca gga aga gaa aga cct cc (SEQ ID NO: 105)	199bp
	2	5'ccc att ctg tgt ttg ggt ttt t (SEQ ID NO: 106)	5'aga ggc tga ggt ggg aga at (SEQ ID NO: 107)	213bp
GSTT1	1	5'gag gtc att ctg aag gcc aag g (SEQ ID NO: 108)	5'ttt gtg gac tgc tga gga cg (SEQ ID NO: 109)	133bp
β-actin	1b	5'tcc tca gat cat tgc tcc (SEQ ID NO: 110)	5'taa cgc aac taa gtc ata gtc c (SEQ ID NO: 111)	175bp
MnSOD	1	5'ggc tgt gct ttc tcg tct tc (SEQ ID NO: 112)	5'ggt gac gtt cag gtt gtt ca (SEQ ID NO: 113)	194bp
	2	5' aca gtg gtt gaa aaa gta gg (SEQ ID NO: 114)	5'caa aat gta gat aag ggt gc (SEQ ID NO: 115)	205bp
ALDH2	1	5'ttg gtg gct aca aga tgt cg (SEQ ID NO: 116)	5'agg tcc tga act tcc agc ag (SEQ ID NO: 117)	345bp
GSTP1	1	5'gct cta tgg gaa gga cca gc (SEQ ID NO: 118)	5' aag cca cct gag ggg taa gg (SEQ ID NO: 119)	192bp
	2	5'cag cag ggt ctc aaa agg (SEQ ID NO: 120)	5'gat gga cag gca gaa tgg (SEQ ID NO: 121)	250bp

Having obtained a sample of DNA, preferably with amplified regions of interest, individual polymorphisms may be identified. Identification of the markers for the polymorphisms involves the discriminative detection of allelic forms of the same gene that differ by nucleotide substitution, or in the case of some genes, for example the GSTM1 and GSTT1 genes, deletion of the entire gene. Methods for the detection of known nucleotide differences are well known to the skilled person. These may include, but are not limited to:

- Hybridization with allele-specific oligonucleotides (ASO), (Wallace, 1981; Ikuta, 1987; Nickerson, 1990, Varlaan, 1986, Saiki, 1989 and Zhang, 1991).
- Allele specific PCR, (Newton 1989, Gibbs, 1989).
- Solid-phase minisequencing (Syvanen, 1993).
- Oligonucleotide ligation assay (OLA) (Wu, 1989, Barany, 1991; Abravaya, 1995).
- The 5' fluorogenic nuclease assay (Holland, 1991 & 1992, Lee, 1998, US patents 4,683,202, 4,683,195, 5,723,591 and 5,801,155).
- Restriction fragment length polymorphism (RFLP), (Donis-Keller, 1987).

In a preferred embodiment, the genetic loci are assessed via a specialised type of PCR used to detect polymorphisms, commonly referred to as the Taqman® assay and performed using an AB7700 instrument (Applied Biosystems, Warrington, UK). In this method, a probe is synthesised which hybridises to a region of interest containing the polymorphism. The probe contains three modifications: a fluorescent reporter molecule, a fluorescent quencher molecule and a minor groove binding chemical to enhance binding to the genomic DNA strand. The probe may be bound to either strand of DNA. For example, in

the case of binding to the coding strand, when the Taq polymerase enzyme begins to synthesise DNA from the 5' upstream primer, the polymerase will encounter the probe and begin to remove bases from the probe one at a time using a 5'-3' exonuclease activity. When the base bound to the fluorescent reporter molecule is removed, the fluorescent molecule is no longer quenched by the quencher molecule and the molecule will begin to fluoresce. This type of reaction can only take place if the probe has hybridised perfectly to the matched genomic sequence. As successive cycles of amplification take place, i.e. more probes and primers are bound to the DNA present in the reaction mixture, the amount of fluorescence will increase and a positive result will be detected. If the genomic DNA does not have a sequence that matches the probe perfectly, no fluorescent signal is detected.

Examples of oligonucleotide probes which may be used in the invention, particularly when the Taqman® assay is used in the method of the invention together with primers which may be used. These oligonucleotide probes form another aspect of the present invention.

Therefore in a further aspect of the invention, there is provided an oligonucleotide having a sequence selected from SEQ ID NO: 164-202. The invention further provides a set of oligonucleotides comprising at least 5, 10, 20, 30, 40, 50, 60 or 70 oligonucleotides selected from the group comprising SEQ ID NO:164-202.

Arrays

In a preferred embodiment of the invention, hybridisation with allele specific oligonucleotides is conveniently carried out

using oligonucleotide arrays, preferably microarrays, to determine the presence of particular polymorphisms.

Such microarrays allow miniaturisation of assays, e.g. making use of binding agents (such as nucleic acid sequences) immobilised in small, discrete locations (microspots) and/or as arrays on solid supports or on diagnostic chips. These approaches can be particularly valuable as they can provide great sensitivity (particularly through the use of fluorescent labelled reagents), require only very small amounts of biological sample from individuals being tested and allow a variety of separate assays to be carried out simultaneously. This latter advantage can be useful as it provides an assay for different a number of polymorphisms of one or more genes to be carried out using a single sample. Examples of techniques enabling this miniaturised technology are provided in WO84/01031, WO88/1058, WO89/01157, WO93/8472, WO95/18376/ WO95/18377, WO95/24649 and EP-A-0373203, the subject matter of which are herein incorporated by reference.

DNA microarrays have been shown to provide appropriate discrimination for polymorphism detection. Yershov, 1996; Cheung, 1999 and Schena 1999 have described the principles of the technique. In brief, the DNA microarray may be generated using oligonucleotides that have been selected to hybridise with the specific target polymorphism. These oligonucleotides may be applied by a robot onto a predetermined location of a glass slide, e.g. at predetermined X,Y cartesian coordinates, and immobilised. The PCR product (e.g. fluorescently labelled RNA or DNA) is introduced on to the DNA microarray and a hybridisation reaction conducted so that sample RNA or DNA binds to complementary sequences of oligonucleotides in a sequence-specific manner, and allow unbound material to be

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washed away. Gene target polymorphisms can thus be detected by their ability to bind to complementary oligonucleotides on the array and produce a signal. The absence of a fluorescent signal for a specific oligonucleotide probe indicates that the client does not have the corresponding polymorphism. Of course, the method is not limited to the use of fluorescence labelling but may use other suitable labels known in the art. the fluorescence at each coordinate can be read using a suitable automated detector in order to correlate each fluorescence signal with a particular oligonucleotide.

Oligonucleotides for use in the array may be selected to span the site of the polymorphism, each oligonucleotide comprising one of the following at a central location within the sequence:

- wild-type or normal base at the position of interest in the leading strand
- wild-type or normal base at the position of interest in the lag (non-coding) strand
- altered base at the position of interest in the leading strand
- altered complementary base at the position of interest in the lag strand

The arrays used in the present method form another independent aspect of the present invention. Arrays of the invention comprise a set of two or more oligonucleotides, each oligonucleotide being specific to a sequence comprising one or more polymorphisms of a gene selected from the group comprising categories a-k as defined above.

Preferably, the array will comprise oligonucleotides each

being specific to a sequence comprising one or more polymorphisms of an individual gene of at least two different categories a-k as defined above, for example a+b (i.e. at least one oligonucleotide specific for a sequence comprising one or more polymorphisms of a first gene, the first gene being of category a and at least one oligonucleotide specific for a sequence comprising one or more polymorphisms of a second gene, the second gene being of category b), a+c, a+d, a+e, a+f, a+g, a+h, a+i, a+j, a+k, b+c, b+d, b+e etc., c+d, c+e etc, d+e, d+f etc, e+f, e+g etc, f+g, f+h etc., g+h, g+i, g+k, h+i, h+k. Where the array comprises two or more oligonucleotides, it is preferred that at least one of the oligonucleotides is an oligonucleotide specific for a sequence of a polymorphism of a gene of category d, due to the central role of micronutrients in the maintenance of proper cellular growth and DNA repair, and due to the association of micronutrient metabolism or utilisation disorders with several different types of diseases (Ames 1999; Perera, 2000; Potter, 2000). More preferably, the array will comprise oligonucleotides each being specific to a sequence comprising one or more polymorphisms of an individual gene of at least three different categories a-k as defined above, for example, a+b+c, a+b+d, a+b+e, a+b+f, a+b+g, a+b+h, a+b+i, a+b+j, a+b+k a+c+d, a+c+e etc, a+d+e, etc, b+c+d, etc, c+d+e etc, d+e+f etc, and all other combinations of three categories. Where the array comprises three or more oligonucleotides, it is preferred that at least two of the oligonucleotides are oligonucleotides specific for a sequence of a polymorphism of a gene of categories d and e. Information relating to polymorphisms present in both of these categories is particularly useful due to the effects of alcohol consumption and metabolism on the efficiency of enzymes related to micronutrient metabolism and utilisation.(Ulrich, 1999). In a

further preferred embodiment where the array comprises three or more oligonucleotides, it is preferred that at least two of the oligonucleotides are oligonucleotides specific for a sequence of a polymorphism of a gene of c categories a and b due to the close interaction of Phase I and Phase II enzymes in the metabolism of xenobiotics. Even more preferably, the array will comprise oligonucleotides each being specific to a sequence comprising one or more polymorphisms of an individual gene of at least four different categories a-k as defined above, for example, a+b+c+d, a+b+c+e, a+b+d+e, a+c+d+e, b+c+d+e etc. Where the array comprises four or more oligonucleotides, it is preferred that at least three of the oligonucleotides are oligonucleotides specific for a sequence of a polymorphism of a gene of categories d and e and f Information relating to polymorphisms present in these three categories is particularly useful due to the strong correlation of polymorphisms of these alleles with coronary artery disease due to the combined effects of altered micronutrient utilisation, affected adversely by alcohol metabolism, together with imbalances in fat and cholesterol metabolism. Where the array comprises five or more oligonucleotides, it is preferred that at least four of the oligonucleotides are oligonucleotides specific for a sequence of a polymorphism of a gene of categories a, b, d and e. Information relating to polymorphisms present in these four categories is particularly useful due to the combined effects of micronutrients utilisation, alcohol metabolism, Phase 1 metabolism of xenobiotics and Phase II metabolism on the further metabolism and excretion of potentially harmful metabolites produced in the body (Taningher, 1999; Ulrich, 1999). Similarly, the array may comprise oligonucleotides each being specific to a sequence comprising one or more polymorphisms of an individual gene of at least five, for

example a, b, d, e and f, six, seven, eight, nine or ten different categories a-k as defined above.

Most preferably, the array will comprise oligonucleotides each being specific to a sequence comprising one or more polymorphisms of an individual gene of each of categories a-k as defined above.

In one preferred embodiment, the array comprises oligonucleotides each being specific to a sequence comprising one or more polymorphisms of individual genes, the individual genes comprising each member of the group comprising genes encoding cytochrome P450 monooxygenase, N-acetyltransferase 1, N-acetyltransferase 2, glutathione-S-transferase, manganese superoxide dismutase, 5,10-methylenetetrahydrofolatereductase and alcohol dehydrogenase 2 enzymes. genetic loci of genes encoding each of the cytochrome P450 monooxygenase, N-acetyltransferase 1, N-acetyltransferase 2, glutathione-S-transferase, manganese superoxide dismutase, 5,10-methylenetetrahydrofolatereductase and alcohol dehydrogenase 2 enzymes. In a more preferred embodiment the array further comprises oligonucleotides specific for one or more alleles of the genetic loci of genes encoding one or more, preferably each of epoxide hydrolase (EH), NADPH-quinone reductase (NQ01), paraxonaoase (PON1), myeloperoxidase (MPO), alcohol dehydrogenase 1, alcohol dehydrogenase 3, cholesteryl ester transfer protein, apolipoprotein A IV, apolipoprotein E, apolipoprotein C III, angiotensin, factor VII, prothrombin 20210, β-fibrinogen, heme -oxygenase-1, α-antitrypsin, SPINK1, Δ-aminolevulinacid dehydratase, interleukin 1, interleukin 1, vitamin D receptor, B1 kinin receptor, cystathionine-beta-synthase, methionine synthase (B12 MS), 5-HT transporter, transforming growth factor beta 1 (TGFβ1), L-myc, HLA Class 2

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molecules, T-lymphocyte associated antigen 4 (CTLA-4), interleukin 4, interleukin 3, interleukin 6, IgA, and/or galactose metabolism gene GALT.

In preferred arrays, the oligonucleotides in the array comprise at least 5, 10, 20, 30, 40, 50, 60 or 70 oligonucleotides selected from the group comprising SEQ ID NO:1 - SEQ ID NO: 85 illustrated in TABLE 3 which shows preferred oligonucleotides listed in the right column with the primer set used to amplify the appropriate fragments of sample DNA listed in the left column.

In a preferred embodiment the array will comprise all of the oligonucleotides SEQ ID NO:1 - 85.

Table 3

Gene Target	25 nt sequence
1. CYP1A1	
Primer set1 A4889G wt-lead	5' atc ggt gag acc Att gcc cgc tgg g (SEQ ID NO: 1)
Primer set1 A4889G wt-lag	5' ccc agc ggg caa Tgg tct cac cga t (SEQ ID NO: 2)
Primer set1 A4889G polymorph-lead	5' atc ggt gag acc Gtt gcc cgc tgg g (SEQ ID NO: 3)
Primer set1 A4889G polymorph- lag	5' ccc agc ggg caa Cgg tct cac cga t (SEQ ID NO: 4)
Primer set2 T6235C wt-lead	5' acc tcc acc tcc Tgg gct cac acg a (SEQ ID NO: 5)
Primer set2 T6235C wt-lag	5' tcg tgt gag ccc Agg agg tgg agg t (SEQ ID NO: 6)
Primer set2 T6235C polymorph-lead	5' acc tcc acc tcc Cgg gct cac acg a (SEQ ID NO: 7)

Gene Target	25 nt sequence
Primer set2 T6235C polymorph-lag	5' tcg tgt gag ccc Ggg agg tgg agg t (SEQ ID NO: 8)
2. NAT1	
Primer set1	N/A
Primer set2	N/A
Primer set 3 G445A wt-lead	5'cag gtg cct tgt Gtc ttc cgt ttg a (SEQ ID NO: 9)
Primer set3 G445A wt-lag	5' tca aac gga aga Cac aag gca cct g (SEQ ID NO: 10)
Primer set3 G445A polymorph-lead	5' cag gtg cct tgt Atc ttc cgt ttg a (SEQ ID NO: 11)
Primer set3 G445A polymorph-lag	5' tca aac gga aga Tac aag gca cct g (SEQ ID NO: 12)
Primer set3 G459A wt-lead	5' ctt ccg ttt gac Gga aga gaa tgg a (SEQ ID NO: 13)
Primer set3 G459A wt-lag	5' tcc att ctc ttc Cgt caa acg gaa g (SEQ ID NO: 14)
Primer set3 G459A polymorph-lead	5' ctt ccg ttt gac Aga aga gaa tgg a (SEQ ID NO: 15)
Primer set3 G459A polymorph-lag	5' tcc att ctc ttc Tgt caa acg gaa g(SEQ ID NO: 16)
Primer set4 G560A wt-lead	5' aca gca aat acc Gaa aaa tct act c (SEQ ID NO: 17)
Primer set4 G560A wt-lag	5' gag tag att ttt Cgg tat ttg ctg t (SEQ ID NO: 18)
Primer set4 G560A polymorph-lead	5' aca gca aat acc Aaa aaa tct act c (SEQ ID NO: 19)
Primer set4 G560A polymorph-lag	5' gag tag att ttt Tcc tat ttg ctg t (SEQ ID NO: 20)
Primer set5T1088A wt-lead*a	5' taa taa taa taa Taa atg tct ttt a (SEQ ID NO: 21)
Primer set5 T1088A wt-lag*a	5' taa aag aca ttt Att att att att a

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Gene Target	25 nt sequence
	(SEQ ID NO: 22)
Primer set5T1088A wt-lead*b	5' taa taa taa taa Taa atg tat ttt a (SEQ ID NO: 23)
Primer set5 T1088A wt-lag*b	5' taa aat aca ttt Att att tta att a (SEQ ID NO: 24)
Primer set5 T1088Apolymorph-lead*a	5' taa taa taa taa Aaa atg tct ttt a (SEQ ID NO: 25)
Primer set5 T1088A polymorph-lag*a	5' taa aag aca ttt Ttt att tta att a (SEQ ID NO: 26)
Primer set5 T1088Apolymorph-lead*b	5' taa taa taa taa Aaa atg tat ttt a (SEQ ID NO: 205)
Primer set5 T1088A polymorph-lag*b	5' taa aat aca ttt Ttt att tta att a (SEQ ID NO: 27)
*redundancy due to adjacent polymorphisms	
Primer set5 C1095A wt-lead*a	5' aat aat aaa tgt Ctt tta aag atg g (SEQ ID NO: 28)
Primer set5 C1095A wt-lag*a	5' cca tct tta aaa Gac att tat tat t (SEQ ID NO: 29)
Primer set5 C1095A wt-lead*b	5' aat aaa aaa tgt Ctt tta aag atg g (SEQ ID NO: 30)
Primer set5 C1095A wt-lag*b	5' cca tct tta aaa Gac att ttt tat t (SEQ ID NO: 31)
Primer set5 C1095Apolymorph-lead*a	5' aat aat aaa tgt Att tta aag atg g (SEQ ID NO: 32)
Primer set5 C1095A polymorph-lag*a	5' cca tct tta aaa Tac att tat tat t (SEQ ID NO: 33)
Primerset5 C1095Apolymorph-lead*b	5' aat aaa aaa tgt Att tta aag atg g (SEQ ID NO: 34)
Primer set5 C1095A polymorph-lag*b	5' cca tct tta aaa Tac att ttt tat t (SEQ ID NO: 35)
*redundancy due to adjacent polymorphisms	
3. **NAT2**	
Primer set1 C282T wt-lead	5' agg gta ttt tta Cat ccc tcc agt t

Gene Target	25 nt sequence
	(SEQ ID NO: 36)
Primer set1 C282T wt-lag	5' aac tgg agg gat Gta aaa ata ccc t (SEQ ID NO: 37)
Primer set1 C282T polymorph-lead	5' agg gta ttt tta Tat ccc tcc agt t (SEQ ID NO: 38)
Primer set1 C282T polymorph-lag	5' aac tgg agg gat Ata aaa ata ccc t (SEQ ID NO: 39)
Primer set2 C481T wt-lead	5' gga atc tgg tac Ctg gac caa atc a (SEQ ID NO: 40)
Primer set2 C481T wt-lag	5' tga ttt ggt cca Ggt acc aga ttc c (SEQ ID NO: 41)
Primer set2 C481T polymorph-lead	5' gga atc tgg tac Ttg gac caa atc a (SEQ ID NO: 42)
Primer set2 C481T polymorph-lag	5' tga ttt ggt cca Agt acc aga ttc c (SEQ ID NO: 43)
Primer set2 G590A wt-lead	5' cgc ttg aac ctc Gaa caa ttg aag a (SEQ ID NO: 44)
Primer set2 G590A wt-lag	5' tct tca att gtt Cga ggt tca agc g (SEQ ID NO: 45)
Primer set2 G590A polymorph-lead	5' cgc ttg aac ctc Aaa caa ttg aag a (SEQ ID NO: 46)
Primer set2 G590A polymorph-lag	5' tct tca att gtt Tga ggt tca agc g (SEQ ID NO: 47)
Primer set3 G857A wt-lead	5' aac ctg gtg atg Gat ccc tta cta t (SEQ ID NO: 48)
Primer set3 G857A wt-lag	5' ata gta agg gat Cca tca cca ggt t (SEQ ID NO: 49)
Primer set3 G857A polymorph-lead	5' aac ctg gtg atg Aat ccc tta cta t (SEQ ID NO: 50)
Primer set3 G857A polymorph-lead	5' ata gta agg gat Tca tca cca ggt t (SEQ ID NO: 51)
4. **GSTM1**	

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Gene Target	25 nt sequence
Primer set1 wt-lead	5'gct aca ttg ccc gca agc aca acc t (SEQ ID NO: 52)
Primer set1 wt-lag	5' agg ttg tgc ttg cgg gca atg tag c (SEQ ID NO: 53)
5. GSTP1	
Primer set1 A313G wt-lead	5' cgc tgc aaa tac Atc tcc ctc atc t (SEQ ID NO: 54)
Primer set1 A313G wt-lag	5' aga tga ggg aga Tgt att tgc agc g (SEQ ID NO: 55)
Primer set1 A313G polymorph-lead	5' cgc tgc aaa tac Gtc tcc ctc atc t (SEQ ID NO: 56)
Primer set1 A313G polymorph-lag	5' aga tga ggg aga Cgt att tgc agc g (SEQ ID NO: 57)
Primer set2 C341T wt-lead	5' tct ggc agg agg Cgg gca agg atg a (SEQ ID NO: 58)
Primer set2 C341T wt-lag	5' tca tcc ttg ccc Gcc tcc tgc cag a (SEQ ID NO: 59)
Primer set2 C341T polymorph-lead	5' tct ggc agg agg Tgg gca agg atg a (SEQ ID NO: 60)
Primer set2 C341T polymorph-lag	5' tca tcc ttg ccc Acc tcc tgc cag a (SEQ ID NO: 61)
6. GSTT1	
Primer set1 wt-lead	5' acc ata aag cag aag ctg atg ccc t (SEQ ID NO: 62)
Primer set2 wt-lag	5' agg gca tca gct tct gct tta tgg t (SEQ ID NO: 63)
7. MnSOD	
Primer set1 T-26C wt-lead	5' agc tgg ctc cgg Ttt tgg ggt atc t (SEQ ID NO: 64)
Primer set1 T-26Cwt lag	5' aga tac ccc aaa Acc gga gcc agc t (SEQ ID NO: 65)
Primer set1 T-26C polymorph -lead	5' agc tgg ctc cgg Ctt tgg ggt atc t (SEQ ID NO: 66)

Gene Target	25 nt sequence
Primer set1 T-26C polymorph - lag	5' aga tac ccc aaa Gcc gga gcc agc t (SEQ ID NO: 67)
Primer set2 T175C wt-lead	5' tta cag ccc aga Tag ctc ttc agc c (SEQ ID NO: 68)
Primer set2 T175C wt-lag	5' ggc tga aga gct Atc tgg gct gta a (SEQ ID NO: 69)
Primer set2 T175C polymorph - lead	5' tta cag ccc aga Cag ctc ttc agc c (SEQ ID NO: 70)
Primer set2 T175C polymorph - lag	5' ggc tga aga gct Gtc tgg gct gta a (SEQ ID NO: 71)
8. MTHFR	
Primer set1 C677T wt - lead	5' tgt ctg cgg gag Ccg att tca tca t (SEQ ID NO: 72)
Primer set1 C677T wt- lag	5' atg atg aaa tcg Gct ccc gca gac a (SEQ ID NO: 73)
Primer set1 C677T polymorph - lead	5' tgt ctg cgg gag Tcg att tca tca t (SEQ ID NO: 74)
Primer set1 C677T polymorph- lag	5' atg atg aaa tcg Act ccc gca gac a (SEQ ID NO: 75)
Primer set2 A1298C wt-lead	5' tga cca gtg aag Aaa gtg tct ttg a (SEQ ID NO: 76)
Primer set2 A1298C wt-lag	5' tca aag aca ctt Tct tca ctg gtc a (SEQ ID NO: 77)
Primer set2 A1298C polymorph-lead	5' tga cca gtg aag Caa gtg tct ttg a (SEQ ID NO: 78)
Primer set2 A1298C polymorph-lag	5' tca aag aca ctt Gct tca ctg gtc a (SEQ ID NO: 79)
9. ALDH2	
Primer set1 wt-lead	5' cag gca tac act Gaa gtg aaa act g (SEQ ID NO: 80)
Primer set 1 wt-lag	5' cag ttt tca ctt Cag tgt atg cct g (SEQ ID NO: 81)

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Gene Target	25 nt sequence
Primer set1 polymorph-lead	5' cag gca tac act Aaa gtg aaa act g (SEQ ID NO: 82)
Primer set 1 polymorph-lag	5' cag ttt tca ctt Tag tgt atg cct g (SEQ ID NO: 83)
10. beta-Actin	
Primer set 1 -lead	5' tgc atc tct gcc tta cag atc atg t (SEQ ID NO: 84)
Primer set1-lag	5' aga tga tct gta agg cag aga tgc a (SEQ ID NO: 85)

Advice decision tree

The results of genetic polymorphism analysis may be used to correlate the genetic profile of the donor of the sample with disease susceptibility using the first dataset, which provides details of the relative disease susceptibility associated with particular polymorphisms and their interactions. The risk factors identified using dataset 1 can then be matched with dietary and other lifestyle recommendations from dataset 2 to produce a lifestyle advice plan individualised to the genetic profile of the donor of the sample. Examples of datasets 1 and 2 which may be used to generate such advice is illustrated in Figure 1.

To enable appropriate advice to be tailored to particular susceptibilities, a ranking system is preferably used to provide an indication of the degree of susceptibility of a specific polymorph to risk of cancer(s) and/or other conditions. The ranking system may be designed to take into account of homozygous or heterozygous alleles in the client's

sample, i.e. the same or different alleles being present in diploid nucleus. Five categories which may be used are summarised below:

(i) Reduced susceptibility: where an allele has been shown to reduce susceptibility.

(ii) Normal susceptibility: where allele has been shown to have a normal susceptibility of risk to cancer(s) or disease. This is generally the homozygous wild type allele or a polymorphism that has been shown to have similar function.

(iii) Moderate susceptibility: where a heterozygous genotype is present that contains the wild type of the allele (i.e. normal susceptibility) and an allele of the polymorphism known to give rise to higher susceptibility to specific cancer(s) or disease.

(iv) High susceptibility: where a homozygous genotype that contains the polymorphism is present with a higher risk of cancer susceptibility.

(v) Higher susceptibility: where a higher susceptibility has been observed for specific cancer(s) or disease due to the combined effects of two or more different gene targets.

Using dataset 1, a susceptibility may be assigned to each polymorphism identified and, from dataset 2, a lifestyle recommendation corresponding to each susceptibility identified may be assigned. For example, if an individual is found to have the NAT1*10 polymorphism, the decision tree may indicate that the there is an enhanced susceptibility of colonic cancer. Recommendations appropriate to minimising the risk of colonic cancer are then generated. For example, the

recommendations may be to avoid particular foods associated with increased risk and to increase consumption of other foods associated with a protective effect against such cancers. The totality of recommendations may be combined to generate a lifestyle advice plan individualised to the donor of the sample. The decision tree is preferably arranged to recognise particular combinations of polymorphisms and/or susceptibilities which interact either positively to produce a susceptibility greater than would be expected from the risk factors associated with each individually, and/or, which interact negatively to reduce the susceptibility associated with each individually. Where such combinations are identified, the advice generated can be tailored accordingly. For example, the combination of NAT2*4 and NAT1*10 polymorphisms have been linked to increased cancer risk (Bell, 1995). Therefore, when such a combination of polymorphisms is identified from a subject's DNA, the associated very high susceptibility to cancer is assigned and the advice tailored to emphasise the need to reduce consumption of xenobiotics, e.g. by reducing or eliminating consumption of char-grilled foodstuffs.

In generating the advice, other factors such as information concerning the sex and health of the individual and /or of the individual's family, age, alcohol consumption, and existing diet may be used in the determination of appropriate lifestyle recommendations.

Experimental

Example 1 Preparation of DNA Sample

DNA is prepared from a buccal cell sample on a brush using a Qiagen QIAamp kit according to the manufacturer's instructions

(Qiagen, Crawley, UK). Briefly, the brush is cut in half and one half stored at room temperature in a sealed tube in case retesting is required. The other half of the brush is placed in a microcentrifuge tube. 400µl PBS is added and the brush allowed to rehydrate for 45 minutes at room temperature. Quiagen lysis buffer and Proteinase K is then added, the contents are mixed, and allowed to incubate at 56 C for 15 minutes to lyse the cells. Ethanol is added and the lysate transferred to a QIAamp spin column from which DNA is eluted after several washings.

Example 2 Quantification of DNA

In order to check that sufficient DNA has been isolated, a quantification step is carried out using the PicoGreen dsDNA Quantification kit (Molecular Probes, Eugene, Oregon, USA).

Briefly, client DNA samples are prepared by transferring a 10 µl aliquot into a microcentrifuge tube with 90µl TE. 100 µl of the working PicoGreen dsDNA quantification reagent is added, mixed well, and transferred into a black 96 well plate with flat well bottoms. The plate is then incubated for 5 minutes in the dark before a fluorescent reading is taken. The quantity of DNA present in the clients' samples is determined by extrapolating from a calibration plot prepared using DNA standards.

A quantity of DNA in the range of 5-50ng total is used in the subsequent PCR step. Remaining client DNA sample is stored at -20°C for retesting if required.

Example 3 Taqman® Assay to Identify the MTHFR A1298C polymorphism

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The modified reaction mixture contains Taq polymerase (1.25 units/µl), optimised PCR buffer, dNTP (200µM each), 2mM $MgCl_2$ and primer pairs SEQ ID NO: 160 and 161 and polymorphism probe SEQ ID NO: 200.

The reaction mixture is initially incubated for 10 minutes at 50°C, then 5 minutes at 95°C, followed by 40 cycles of 1 minute of annealing at between 55°C and 60°C and 30 seconds of denaturation at 95°C. Both during the cycles and at the end of the run, fluorescence of the released reporter molecules of the probe is measured by an integral CCD detection system of the AB7700 thermocycler. The presence of a fluorescent signal which increases in magnitude through the course of the run indicates a positive result.

The assay is then repeated with the same primer pair and wt probe SEQ ID NO: 199. If the sample is homozygous for the polymorphism, no fluorescence signal is seen with the wt probe. However, if the sample is heterozygous for the polymorphism, a fluorescence signal is also seen with the wt probe. If single reporter results from homozygous wt, homozygous polymorphic and heterozygous polymorphic samples are plotted are plotted on an X/Y axis, the homozygous alleles will cluster at opposite ends of the axes relative to each reporter, and the heterozygous alleles will cluster at a midway region.

__Example 4__ DNA Array method for identifying polymorphisms for Identifying multiple polymorphisms

a) PCR amplification

The PCR reaction mix contains Taq polymerase (1.25

units/reaction), optimised PCR buffer, dNTP's (200µM each) and $MgCl_2$ at an appropriate concentration of between 1 and 4 mM, and 40 pmol of each primer(SEQ ID NOS: 1-8, 17-63) for amplification of seven fragments and the sample DNA.

The reaction mixture is initially incubated at 95°C for 1 minute, and then subjected to 45 cycles of PCR in a MWG TC9600 thermocycler (MWG-Biotech-AG Ltd., Milton Keynes, UK) as follows:
annealing 50°C, 1 minute
polymerisation 73°C., 1 minute
denaturation 95°C., 30 seconds.
After a further annealing step at 50°C, 1 minute, there is a final polymerisation step at 73°C for 7 minutes.

(Instead of the MWG TC9600 thermocycler, other thermocyclers, such as the Applied Biosystems 9700 thermocycler (Applied Biosystems, Warrington, UK), may be used.

After amplification of the target genes, generation of product is checked by electrophoresis separation using 2% agarose gel, or a 3.5% NuSieve agarose gel.

The PCR mplification products are then purified using the Qiagen QIAquick PCR Purification Kit (Qiagen, Crawley, UK) to remove dNTPs, primers, and enzyme from the PCR product. The PCR product is layered onto a QIAquick spin column, a vacuum applied to separate the PCR product from the other reaction products and the DNA eluted in buffer.

b) RNA transcription and Fluorescent Labelling of PCR products

The DNA is then transcribed into RNA using T3 and T7 RNA

polymerases together with fluorescently labelled UTP for incorporation into the growing chain of RNA. The reaction mixture comprises:
20µl 5X reaction buffer; 500µM ATP, CTP, GTP, fluorescent UTP (Amersham Ltd, UK); DEPC treated dH_2O; 1 unit T3 RNA polymerase or 1 unit T7 RNA polymerase (Promega Ltd., Southampton, UK); 1 unit Rnasin ribonuclaese inhibitor and DNA from PCR (1/3 of total, 10µl in dH_2O).

The mixture is incubated at 37°C for 1 hour. The mixture is then treated with DNAse to remove DNA so that only newly synthesised fluorescent RNA is left. The RNA is then precipitated, microcentrifuged and resuspended in buffer for hybridisation on the array.

c) Polymorphism Analysis

The sample amplified fragments are then tested using a DNA microarray

The DNA microarray used comprises oligonucleotides SEQ ID NOs: 1-85. These oligonucleotides are applied by a robot onto a glass slide and immobilised. The fluorescently labelled amplified DNA is introduced onto the DNA microarray and a hybridisation reaction conducted to bind any complementary sequences in the sample, allowing unbound material to be washed away. The presence of bound samples is detected using a scanner. The absence of a fluorescent signal for a specific oligonucleotide probe indicates that the client does not have the corresponding polymorphism.

__Example 5__ DNA Array method for identifying G560A polymorphism

The PCR reaction mix contains Taq polymerase (1.25 units/reaction), optimised PCR buffer, dNTP's (200µM each) and $MgCl_2$ at an appropriate concentration of between 1 and 4 mM, and 40 pmol of each primer (SEQ ID NOs: 88,89) for amplification of the fragment. The methods used is the same as detailed in Example 4, with the array comprising oligonucleotides SEQ ID NO: 17, 18, 19 and 20.

The presence of bound samples is detected using a scanner as described above. A highly fluorescent spot is detected at the positions corresponding to the oligonucleotides SEQ ID NO: 19 and 20. No signal is seen at the spots corresponding to SEQ ID NO: 17 and 18, demonstrating that the sample is not heterozygous for the wt allele.

__Example 6__ Generation of Report

The results of the microarray or Taqman® analysis are input into a computer comprising a first dataset correlating the presence of individual alleles with a risk factor and a second dataset correlating risk factors with lifestyle advice. A report is generated identifying the presence of particular polymorphisms and providing lifestyle recommendations based on the identified polymorphisms. An example of such a decision process is shown in Figure 2.

A sample of DNA is screened and the alleles identified input to a dataprocessor as Dataset 3. Each allele is matched to lifestyle risk factor from dataset 1, e.g. high susceptibility to colon cancer due to the presence of the NAT1*10 allele and the absence of the GSTM1 allele. The identified risk factor is then matched with one or more lifestyle recommendations from dataset 2, for example "avoid red meat, chargrilled food,

smoked meats and fish; stop smoking immediately" (in order to avoid production of potentially toxic byproducts by Phase 1 enzymes with increased activity) and "increase consumption of vegetables of the allium family e.g. onions and garlic, and the brassaicae family e.g. broccoli" (in order to increase the activity of Phase 11 enzymes present, such as GSTP1 and GSTT1 and others, in order to increase the excretion of toxic byproducts of Phase 1 metabolism). This is then checked against other factors input into the dataprocessor, e.g. age, sex and existing diet to modify the recommendation accordingly before generating the final recommendation appropriate to the allele. The lifestyle recommendations are then assembled to generate a comprehensive personalised lifestyle advice plan.

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CLAIMS:

1. A computer assisted method of providing a personalized lifestyle advice plan for a human subject comprising:

(i) providing a first dataset on a data processing means, said first dataset comprising information correlating the presence of individual alleles at genetic loci with a lifestyle risk factor, wherein at least one allele of each genetic locus is known to be associated with increased or decreased disease susceptibility;

(ii) providing a second dataset on a data processing means, said second dataset comprising information matching each said risk factor with at least one lifestyle recommendation;

(iii)inputting a third dataset identifying alleles at one or more of the genetic loci of said first dataset of said human subject;

(iv) determining the risk factors associated with said alleles of said human subject using said first dataset;

(v) determining at least one appropriate lifestyle recommendation based on each identified risk factor from step (iv) using said second dataset; and

(vi) generating a personalized lifestyle advice plan based on said lifestyle recommendations.

2. The method according to the method of claim 1 wherein the personalised lifestyle advice plan includes recommended minimum and/or maximum amounts of food subtypes.

3. The method according to claim 1 or claim 2 wherein the method comprises the step of delivering the report to the client.

4. The method according to claim 3 wherein the plan is

delivered via the Internet and accessible via a unique identifier code.

5. The method according to claim 4 wherein the plan comprises hyperlinks to one or more Web pages.

6. The method according to any one of claims 1 to 5 wherein said first dataset comprises information relating to two or more alleles of one or more genetic loci of genes selected from the group comprising:

(a) genes that encode enzymes responsible for detoxification of xenobiotics in Phase I metabolism;

(b) genes that encode enzymes responsible for conjugation reactions in Phase II metabolism;

(c) genes that encode enzymes that help cells to combat oxidative stress;

(d) genes associated with micronutrient deficiency; and

(e) genes that encode enzymes responsible for metabolism of alcohol.

(f) genes that encode enzymes involved in lipid and/or cholesterol metabolism;

(g) genes that encode enzymes involved in clotting;

(h) genes that encode trypsin inhibitors;

(i) genes that encode enzymes related to susceptibility to metal toxicity;

(j) genes which encode proteins required for normal cellular metabolism and growth; and

(k) genes which encoded HLA Class 2 molecules.

7. The method according to claim 6 wherein said first dataset comprises information relating to two or more alleles of one or more genetic loci of genes selected from each member of the group comprising:

(a) genes that encode enzymes responsible for detoxification of xenobiotics in Phase I metabolism;

(b) genes that encode enzymes responsible for conjugation reactions in Phase II metabolism;

(c) genes that encode enzymes that help cells to combat oxidative stress;

(d) genes associated with micronutrient deficiency; and

(e) genes that encode enzymes responsible for metabolism of alcohol.

(f) genes that encode enzymes involved in lipid and/or cholesterol metabolism;

(g) genes that encode enzymes involved in clotting;

(h) genes that encode trypsin inhibitors;

(i) genes that encode enzymes related to susceptibility to metal toxicity;

(j) genes which encode proteins required for normal cellular metabolism and growth; and

(k) genes which encoded HLA Class 2 molecules.

8. The method according to claim 6 wherein said first dataset comprises information relating to two or more alleles of one or more genetic loci of genes encoding an enzyme selected from the group comprising: cytochrome P450 monooxygenase, N-acetyltransferase 1 , N-acetyltransferase 2, glutathione-S-transferase, manganese superoxide dismutase, 5,10-methylenetetrahydrofolatereductase and alcohol dehydrogenase 2.

9. The method according to claim 8 wherein said first dataset comprises information relating to two or more alleles of one or more genetic loci of each of the genes encoding cytochrome P450 monooxygenase, N-acetyltransferase 1, N-acetyltransferase 2, glutathione-S-transferase, manganese superoxide dismutase,

5,10-methylene-tetrahydrofolatereductase and alcohol dehydrogenase 2.

10. The method according to any one of claims 1 to 9 including the step of determining the presence of individual alleles at one or more genetic loci of the DNA in a DNA sample of said human subject, and constructing the dataset used in step (iii) using results of said determination.

11. The method according to claim 10 wherein said presence of said individual alleles is determined by hybridisation with allele-specific oligonucleotides.

12. The method according to claim 11 wherein said allele specific oligonucleotides are selected from oligonucleotides each specific for one of the genes selected from the group comprising the CYP1A1 gene, the GSTμ gene, the GSTπ gene, the GSTθ gene, the NAT1 gene, the NAT2 gene, the MnSOD gene, the MTHFR gene and the ALDH2 gene.

13. A microarray comprising a plurality of oligonucleotides, each oligonucleotide being specific to a sequence comprising one or more polymorphisms of a gene selected from the group of:

(a) genes that encode enzymes responsible for detoxification of xenobiotics in Phase I metabolism;

(b) genes that encode enzymes responsible for conjugation reactions in Phase II metabolism;

(c) genes that encode enzymes that help cells to combat oxidative stress;

(d) genes associated with micronutrient deficiency; and

(e) genes that encode enzymes responsible for metabolism of alcohol.

(f) genes that encode enzymes involved in lipid and/or cholesterol metabolism;

(g) genes that encode enzymes involved in clotting;

(h) genes that encode trypsin inhibitors;

(i) genes that encode enzymes related to susceptibility to metal toxicity;

(j) genes which encode proteins required for normal cellular metabolism and growth; and

(k) genes which encoded HLA Class 2 molecules.

14. An array according to claim 13 wherein the array comprises at least oligonucleotides specific to a sequence comprising one or more polymorphisms of a gene selected from (a), (b), (d) and (e).

15. An array according to claim 13 wherein the oligonucleotides comprise at least 40 oligonucleotides selected from the group SEQ ID NO:1-85 and 205.

16. An array comprising the oligonucleotides SEQ ID NO:1-85 and 205.

17. A set of at least 5 primer pairs comprising a plurality of oligonucleotides, each primer pair being capable of detecting a polymorphism in a gene selected from the group of:

(a) genes that encode enzymes responsible for detoxification of xenobiotics in Phase I metabolism;

(b) genes that encode enzymes responsible for conjugation reactions in Phase II metabolism;

(c) genes that encode enzymes that help cells to combat oxidative stress;

(d) genes associated with micronutrient deficiency; and

(e) genes that encode enzymes responsible for metabolism

of alcohol.

(f) genes that encode enzymes involved in lipid and/or cholesterol metabolism;

(g) genes that encode enzymes involved in clotting;

(h) genes that encode trypsin inhibitors;

(i) genes that encode enzymes related to susceptibility to metal toxicity;

(j) genes which encode proteins required for normal cellular metabolism and growth; and

(k) genes which encoded HLA Class 2 molecules.

18. The set of claim 17 which comprises primer pairs capable of detecting a gene in at least five of the categories (a) to (k).

19. A set according to claim 17 or 18 wherein the set comprises at least one primer pair of SEQ ID NO:n and SEQ ID NO:(n+1), where n is an even number from 86 to 98 or 104 to 162.

20. A method of profiling an individual's risk factors to dietary and environmental factors which method comprises bringing a sample of the individual's DNA into contact with an array according to any one of claims 13 to 16 or set of primer pairs according to any one of claims 17 to 19, determining the presence or absence of alleles of genes detectable by said array or pairs associated with risk factors present in the individual, and performing the method of any one of claims 1 to 12.

FIGURE 1

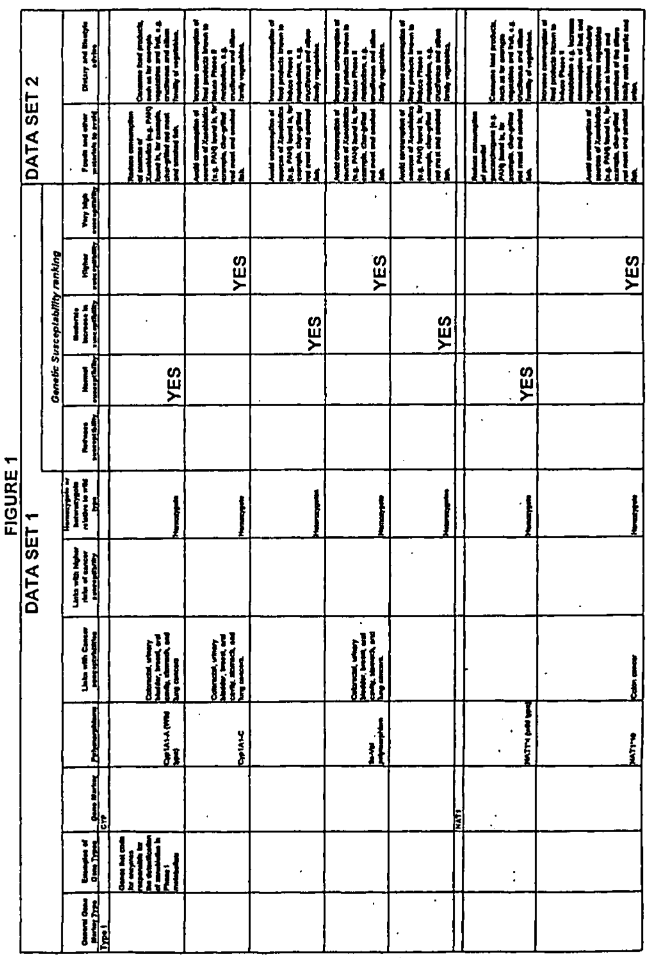

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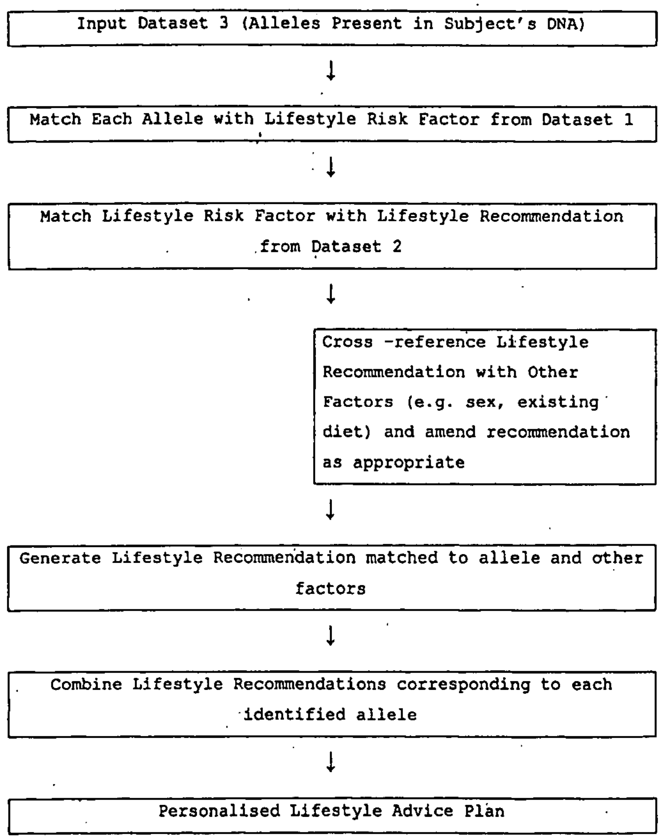
Figure 2


Input Dataset 3 (Alleles Present in Subject's DNA)
Match Each Allele with Lifestyle Risk Factor from Dataset 1
Match Lifestyle Risk Factor with Lifestyle Recommendation from Dataset 2
Cross -reference Lifestyle Recommendation with Other Factors (e.g. sex, existing diet) and amend recommendation as appropriate
Generate Lifestyle Recommendation matched to allele and other factors
Combine Lifestyle Recommendations corresponding to each identified allele
Personalised Lifestyle Advice Plan